

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:27:29 ; Search time 121.018 Seconds
(without alignments)
281.578 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566

Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQSNMPTFGCSTKVEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	476	84.1	108	Q9UL77	Q9UL77 homo sapien
2	465.5	82.2	107	Q96SA9	Q96SA9 homo sapien
3	457	80.7	236	Q7Z3Y4	Q7Z3Y4 homo sapien
4	456	80.6	108	Q9UL70	Q9UL70 homo sapien
5	448.5	79.2	107	Q9UL81	Q9UL81 homo sapien
6	434	76.7	234	Q7Z473	Q7Z473 homo sapien
7	433	76.5	108	Q9UL79	Q9UL79 homo sapien
8	421	74.4	108	Q9UL83	Q9UL83 homo sapien
9	420	74.2	116	Q96PF6	Q96PF6 homo sapien
10	407.5	72.0	109	Q9UL85	Q9UL85 homo sapien
11	405	71.6	234	Q91WF8	Q91WF8 mus musculu
12	405	71.6	234	Q8R062	Q8R062 mus musculu
13	401	70.8	108	Q8VJ30	Q8VJ30 mus musculu
14	396	70.0	233	Q91WS9	Q91WS9 mus musculu
15	393	69.4	109	Q920E6	Q920E6 mus musculu
16	392	69.3	214	Q9RIAS	Q9RIAS mus musculu

17	390	68.9	236	11	Q7TWK3	Q7TWK3 mus musculu
18	389	68.7	238	11	Q9OYF0	Q9OYF0 mus musculu
19	387	68.4	234	11	Q8VCP0	Q8VCP0 mus musculu
20	386.5	68.3	109	4	Q9UL78	Q9UL78 homo sapien
21	384	67.8	236	11	Q7TS98	Q7TS98 mus musculu
22	383	67.7	107	11	Q9UL84	Q9UL84 mus musculu
23	378	66.8	111	11	Q920E9	Q920E9 mus musculu
24	374.5	66.2	114	11	Q8K1F1	Q8K1F1 mus musculu
25	368.5	65.1	109	4	Q9UL86	Q9UL86 homo sapien
26	367.5	64.9	112	11	Q8K1F3	Q8K1F3 mus musculu
27	366.5	64.8	112	11	Q8K1F2	Q8K1F2 mus musculu
28	363.5	64.2	243	11	Q7TQM2	Q7TQM2 mus musculu
29	362	64.0	127	11	Q92S59	Q92S59 mus musculu
30	361	63.8	111	11	Q81IU6	Q81IU6 mus musculu
31	360.5	63.7	134	11	Q8VDD0	Q8VDD0 mus musculu
32	354	62.5	99	11	Q9UL74	Q9UL74 mus musculu
33	352.5	62.3	238	11	Q99M37	Q99M37 mus musculu
34	350	61.8	131	11	Q81IC3	Q81IC3 mus musculu
35	348.5	61.6	238	11	Q8VC16	Q8VC16 mus musculu
36	345	61.0	107	11	Q9ERZ9	Q9ERZ9 mus musculu
37	343	60.6	101	11	Q9JL78	Q9JL78 mus musculu
38	342.5	60.5	106	5	Q9U410	Q9U410 echinocoma
39	342.5	60.5	239	11	Q8VC55	Q8VC55 mus musculu
40	341	60.2	237	13	Q7S236	Q7S236 xenopus lae
41	339.5	60.0	235	11	Q7TWK0	Q7TWK0 mus musculu
42	335.5	59.3	239	4	Q8NEK0	Q8NEK0 homo sapien
43	333.5	58.9	235	11	Q91W12	Q91W12 mus musculu
44	332.5	58.7	112	11	Q8K1F0	Q8K1F0 mus musculu
45	330.5	58.4	239	4	Q8TCD0	Q8TCD0 homo sapien

ALIGNMENTS

RESULT 1
Q9UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77;
AC Q9UL77;
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DT 01-OCT-2003 (TREMURel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; Pubmed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035037; AAD56273.1; -.
DR PIR: B49047; B49047.
DR PIR: S34083; S34083.
DR HSP; P01607; IREI.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716CAD16F3 CRC64;
Query Match 84.1%; Score 476; DB 4; Length 108;
Best Local Similarity 88.0%; Pred. No. 6.7e-46;
Matches 95; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
OY 1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKPKAKPLIYASQISGVPS 60

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Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKAPKLIYHASSLSQSGVPS 60
QY 61 RFSGSGSTDTFTLTISLQPEDPATYTCQGSNSWPTFGQGTVEIKR 108
Db 61 RFSGSGSTDTFTLTISLQPEDPATYTCQGSNSWPTFGQGTVEIKR 108

RESULT 2
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98375893; PubMed=9712075.
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RT J. Immunol. 161:2020-2031(1998).
RL EMBL; U96396; AAB6785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B57F16 CRC64;

Query Match 82.2%; Score 465.5; DB 4; Length 107;
Best Local Similarity 88.9%; Pred. No. 1e-44;
Matches 96; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKLIYHASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKLIYHASSLSQSGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDPATYTCQGSNSWPTFGQGTVEIKR 108
Db 61 RFSGSGSGTDFTLTISLQPEDPATYTCQGSNSWPTFGQGTVEIKR 107

RESULT 3
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
ID Q7Z3Y4
AC Q7Z3Y4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA MEDLINE=2338257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Schieff T.E.,
RA Brownstein M.J., Usdin T.B., Tohyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boufard G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AA05332.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 80.7%; Score 457; DB 4; Length 236;
Best Local Similarity 84.3%; Pred. No. 2.6e-43;
Matches 91; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKLIYHASSLSQSGVPS 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKLIYHASSLSQSGVPS 82

QY 61 RFSGSGSGTDFTLTISLQPEDPATYTCQGSNSWPTFGQGTVEIKR 108
Db 83 RFSGSGSGTDFTLTISLQPEDPATYTCQGSNSWPTFGQGTVEIKR 130

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

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Query Match      80.6%; Score 456; DB 4; Length 108;
Best Local Similarity 85.2%; Pred. No. 1,2e-43;
Matches 92; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSISASVGDRTTTCRASQSISSNNLHWYQKPKAKLLIYHASQISGVPS 60
DB 1 DIQWTGSPSSISASVGDRTTTCRASQSISSNNLHWYQKPKAKLLIYHASQISGVPS 60

QY 61 RFGSGSGCTDFTLTLSLOPEDFATYYCQGSNSMPYFGQTKVEIKR 108
DB 61 RFGSGSGCTDFTLTLSLOPEDFATYYCQGSNSMPYFGQTKVEIKR 108

RESULT 5
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match      79.2%; Score 448.5; DB 4; Length 107;
Best Local Similarity 85.2%; Pred. No. 8.4e-43;
Matches 92; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIQWTGSPSSISASVGDRTTTCRASQSISSNNLHWYQKPKAKLLIYHASQISGVPS 60
DB 1 DIQWTGSPSSISASVGDRTTTCRASQSISSNNLHWYQKPKAKLLIYHASQISGVPS 60

QY 61 RFGSGSGCTDFTLTLSLOPEDFATYYCQGSNSMPYFGQTKVEIKR 108
DB 61 RFGSGSGCTDFTLTLSLOPEDFATYYCQGSNSMPYFGQTKVEIKR 108

RESULT 6
Q7Z473 PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;

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RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Helen F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skalek U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
RW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BABS1BC0F CRC64;

Query Match      76.7%; Score 434; DB 4; Length 234;
Best Local Similarity 80.4%; Pred. No. 1e-40;
Matches 86; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 IQWTGSPSSISASVGDRTTTCRASQSISSNNLHWYQKPKAKLLIYHASQISGVPSR 61
DB 22 IRTGSPSSISASVGDRTTTCRASQSISSNNLHWYQKPKAKLLIYHASQISGVPSR 81

QY 62 RFGSGSGCTDFTLTLSLOPEDFATYYCQGSNSMPYFGQTKVEIKR 108
DB 82 RFGSGSGCTDFTLTLSLOPEDFATYYCQGYTYTPWTFGQTKVEIKR 128

RESULT 7
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1

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FT  NON TER      108      108
SQ  SEQUENCE     108 AA; 11787 MW;  DB5845F19724FB4E CRC64;

Query Match
Best Local Similarity  76.5%; Score 433; DB 4; Length 108;
Matches 88; Conservative 4; Pred.No. 4.8e-41;
Indels 0; Gaps 0;

QY  1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKPKAPKLLIYHASQISGVPS 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKPKAPKLLIYHASQISGVPS 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  61 RFGSGSGGTDFTLTISLTQPEDPATYTCQGSNSWPTFGQGTVEIKR 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  61 RFGSGSGGTDFTLTISLTQPEDPATYTCQGSNSWPTFGQGTVEIKR 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
Q9UL83  PRELIMINARY; PRT; 108 AA.
AC  Q9UL83;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE  Myosin-reactive immunoglobulin light chain variable region
    (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9827139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
    fetus."
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035031; AAD56267.1; -.
DR  PIR; B30609; B30609.
DR  PIR; C30609; C30609.
DR  PIR; D30609; D30609.
DR  PIR; S34098; S34098.
DR  PIR; S34099; S34099.
DR  HSSP; P80362; 1MTL.
DR  InterPro; IPR007110; Ig_1-like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV_1.
DR  SMART; SM00406; IGV_1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER      108      108
SQ  SEQUENCE     108 AA; 11834 MW;  9F9C5A92EBA96EBA CRC64;

Query Match
Best Local Similarity  74.4%; Score 421; DB 4; Length 108;
Matches 77; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY  1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKPKAPKLLIYHASQISGVPS 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1 EIVMTQSPALTSVSPGRATLSGRASGSVSNLAWYQOKPKAPKLLIYASRAIGIRA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  61 RFGSGSGGTDFTLTISLTQPEDPATYTCQGSNSWPTFGQGTVEIKR 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  61 RFGSGSGGTDFTLTISLTQPEDPATYTCQGSNSWPTFGQGTVEIKR 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
Q96PF6  PRELIMINARY; PRT; 116 AA.
AC  Q96PF6;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT  01-OCT-2003 (TREMBLrel. 25, Last annotation update)
```

```
DE  Kappa 1 light chain variable region (Fragment).
GN  SUNK1.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21361171; PubMed=11468171;
RA  Clemenso R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT  "The tropism of organ involvement in primary systemic amyloidosis:
    contributions of Ig V(L) germ line gene use and clonal plasma cell
    burden."
RL  Blood 98:714-720(2001).
DR  EMBL; AF361758; AAK51465.1; -.
DR  InterPro; IPR007110; Ig_1-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV_1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER      116      116
SQ  SEQUENCE     116 AA; 12735 MW;  E796FC2217BFCF57 CRC64;

Query Match
Best Local Similarity  74.2%; Score 420; DB 4; Length 116;
Matches 80; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY  1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKPKAPKLLIYHASQISGVPS 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKPKAPKLLIYDGSFLKTVGS 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  61 RFGSGSGGTDFTLTISLTQPEDPATYTCQGSNSWPTFGQGTVEIKR 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  61 RFGSGSATNFTVLTISLTQPEDPATYTCQYHLLPFTFGPTKVDPKR 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
Q9UL85  PRELIMINARY; PRT; 109 AA.
AC  Q9UL85;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE  Myosin-reactive immunoglobulin kappa chain variable region
    (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9827139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
    fetus."
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035029; AAD56265.1; -.
DR  PIR; D30609; D30609.
DR  HSSP; P80362; 1MTL.
DR  InterPro; IPR007110; Ig_1-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV_1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER      109      109
SQ  SEQUENCE     109 AA; 11761 MW;  FB1E43E7C7AFACCC CRC64;

Query Match
Best Local Similarity  72.0%; Score 407.5; DB 4; Length 109;
Matches 79; Conservative 14; Mismatches 15; Indels 1; Gaps 1;
```


AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013496; AAI13496.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003066; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 70.0%; Score 396; DB 11; Length 233;
Best Local Similarity 71.3%; Pred. No. 1.9e-36;
Matches 77; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISNNLHWYQOKPKAKLLIYHASQSIGVPS 60
Db 20 DIQMTQSPSSLSASVGEIVTITTCRASGNINHWYQOKPKAKLLIYTTSLHSGVPS 79
QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQSNMPTFGQTKVEIKR 108
Db 80 RFGSGSGTDYSLTISNLEPEDIATYCCQRYRLPWTFGGTLKLEIKR 127

RESULT 15
Q920E6 PRELIMINARY; PRT; 109 AA.
AC Q920E6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horatidis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307938; AAL09422.1; -
DR PIR: S19112; S19112.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;

Query Match 69.4%; Score 393; DB 11; Length 109;
Best Local Similarity 70.4%; Pred. No. 1.6e-36;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISNNLHWYQOKPKAKLLIYHASQSIGVPS 60
Db 1 DIQMTQSPSSLSASVGEIVTITTCRASGNINHWYQOKPKAKLLIYTTSLHSGVPS 79
QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQSNMPTFGQTKVEIKR 108
Db 61 RFGSGSGTDYSLTISNLEPEDIATYCCQRYRLPWTFGGTLKLEIKR 127

Search completed: May 13, 2004, 17:01:48
Job time : 122.018 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:27:29 ; Search time 129,982 Seconds
(without alignments)
281.578 Million cell updates/sec

Title: US-09-910-483-5
Perfect score: 617
Sequence: 1 EVGLVBSGGGLVPGGSLRL.....TAGGYWPAWYGGGLTVTVSS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP plant: *
10: SP rodent: *
11: SP virus: *
12: SP vertebrate: *
13: SP unclassified: *
14: SP virus: *
15: SP bacteriap: *
16: SP archaeap: *
17: SP archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441.5	71.6	113	4 Q9UL90	Q9UL90 homo sapien
2	435.5	70.6	116	4 Q9UL93	Q9UL93 homo sapien
3	435.5	70.6	597	4 Q96B89	Q96B89 homo sapien
4	427	69.2	118	4 Q9UL72	Q9UL72 homo sapien
5	427	69.2	613	4 Q8WUK1	Q8WUK1 homo sapien
6	421	68.2	122	4 Q9UL84	Q9UL84 homo sapien
7	419.5	68.0	121	4 Q9UL71	Q9UL71 homo sapien
8	419	67.9	573	4 Q8WU38	Q8WU38 homo sapien
9	417	67.6	112	4 Q9HCC1	Q9HCC1 homo sapien
10	415	67.3	118	4 Q9UL91	Q9UL91 homo sapien
11	415	66.4	494	4 Q96K68	Q96K68 homo sapien
12	409.5	66.4	131	4 Q9UL88	Q9UL88 homo sapien
13	409.5	66.4	499	4 Q8NSK4	Q8NSK4 homo sapien
14	406	65.8	473	11 Q91205	Q91205 mus musculu
15	403.5	65.4	487	11 Q80217	Q80217 mus musculu
16	400.5	64.9	493	4 Q8NCL6	Q8NCL6 homo sapien

17	399.5	64.7	119	11 Q92087	Q92087 mus musculu
18	398	64.5	147	4 Q9Y509	Q9Y509 homo sapien
19	395	64.0	469	11 Q8R3V9	Q8R3V9 mus musculu
20	394.5	63.9	521	4 Q8N4Y9	Q8N4Y9 homo sapien
21	393.5	63.8	470	4 Q7Z5M1	Q7Z5M1 homo sapien
22	390.5	63.3	480	11 Q91XE1	Q91XE1 mus musculu
23	385.5	62.5	479	11 Q91WPS	Q91WPS mus musculu
24	378	61.3	487	11 Q99KX4	Q99KX4 mus musculu
25	375.5	60.9	473	11 Q9DBL4	Q9DBL4 mus musculu
26	372	60.3	479	11 Q7TMC4	Q7TMC4 mus musculu
27	371	60.1	298	11 Q9QYF0	Q9QYF0 mus musculu
28	368	59.6	95	4 Q9ULB6	Q9ULB6 homo sapien
29	363.5	58.9	468	11 Q99L31	Q99L31 mus musculu
30	360.5	58.4	486	11 Q91Z07	Q91Z07 mus musculu
31	360	58.3	484	11 Q8VBA0	Q8VBA0 mus musculu
32	356.5	57.8	109	11 Q9ULB5	Q9ULB5 mus musculu
33	352	57.1	124	4 Q9UL92	Q9UL92 homo sapien
34	345	55.9	437	11 Q9R1A4	Q9R1A4 mus musculu
35	343.5	55.7	119	4 Q9UL94	Q9UL94 homo sapien
36	341.5	55.3	482	4 Q7Z351	Q7Z351 homo sapien
37	341.5	55.3	614	11 Q7TMT6	Q7TMT6 mus musculu
38	339.5	55.0	481	11 Q91WT1	Q91WT1 mus musculu
39	338.5	54.9	104	4 Q9ULB7	Q9ULB7 homo sapien
40	337.5	54.7	125	4 Q9UL95	Q9UL95 homo sapien
41	335.5	54.4	117	11 Q9QXF0	Q9QXF0 mus musculu
42	335	54.3	124	6 Q9N0M4	Q9N0M4 oryctolagus
43	333	54.0	463	11 Q991C4	Q991C4 mus musculu
44	332.5	53.9	146	11 Q924R8	Q924R8 mus musculu
45	332	53.8	124	6 Q9N0W6	Q9N0W6 oryctolagus

ALIGNMENTS

RESULT 1	Q9UL90	PRELIMINARY;	PRT;	113 AA.
AC	Q9UL90;			
DT	01-MAY-2000 (TREMURel. 13, Created)			
DT	01-MAY-2000 (TREMURel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMURel. 25, Last annotation update)			
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).			
DE	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98271139; PubMed=9614934;			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035024; AAD56260.1; -			
DR	HSP; P01772; 2F84			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	PIfam; PF00047; IG; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PSS0835; IG_LIKE; 1.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	113 AA;	12437 MW;	ED57FDD19086D07F CRC64;
Query Match		71.6%;	Score 441.5;	DB 4;
Best Local Similarity		76.7%;	Pred. No. 3.9e-38;	Length 113;
Matches	89;	Conservative	3;	Mismatches 21;
			Indels	3;
			Gaps	1;
QY	1 EVGLVBSGGGLVPGGSLRLSCAAGFNIKDTYIHVVRQAPGKLEWVARIDPANDNTIY 60			
Db	1 EVGLVBSGGGLVPGGSLRLSCAAGFTFSSYGMHWVRQAPGKLEWVARIRYDGSNKY 60			

AC Q8WUJ1;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=tonsil;
 RA Strauberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AA020240.1; -
 DR PIR; P0120; P0120.
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS00835; IG-LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KM Hypothetical protein.
 SO SEQUENCE 613 AA; 67296 MW; 60C75950671E315 CRC64;

Query Match 69.2%; Score 427; DB 4; Length 613;
 Best Local Similarity 71.3%; Pred. No. 1,1e-35;
 Matches 87; Conservative 5; Mismatches 22; Indels 8; Gaps 2;

QY 1 EVOLVESGGGVGGGSLRLSCAAGFNIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
 DB 20 QVQLVSGGSGGVQGRSLRLSCAAGFTFSFGYGMHWRAQPGKLEWVAIVSYGSKNTY 79
 QY 61 ADVSKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYW-----FAYWGQGLTVTV 114
 DB 80 ADVSKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYW-----FAYWGQGLTVTV 137
 QY 115 SS 116
 DB 138 SS 139

RESULT 6

ID Q9UL84 PRELIMINARY; PRT; 122 AA.
 AC Q9UL84;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX [1]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035030; AAD56266.1; -
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 FT NON_TER 1
 FT 1

FT NON TER 122 122
 SO SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 68.2%; Score 421; DB 4; Length 122;
 Best Local Similarity 70.5%; Pred. No. 5.8e-36;
 Matches 86; Conservative 5; Mismatches 25; Indels 6; Gaps 1;

QY 1 EVOLVESGGGVGGGSLRLSCAAGFNIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
 DB 1 EVOLVESGGGVGGGSLRLSCAAGFTFSFGYGMHWRAQPGKLEWVAIVSYGSKNTY 60
 QY 61 ADVSKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYW-----GYWFAWGQGLTVTV 114
 DB 61 ADVSKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYW-----GYWFAWGQGLTVTV 120
 QY 115 SS 116
 DB 121 SS 122

RESULT 7

ID Q9UL71 PRELIMINARY; PRT; 121 AA.
 AC Q9UL71;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX [1]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 FT NON_TER 1
 FT 1
 SO SEQUENCE 121 AA; 13154 MW; 2F045CFA5D50736 CRC64;

Query Match 68.0%; Score 419.5; DB 4; Length 121;
 Best Local Similarity 69.4%; Pred. No. 8.3e-36;
 Matches 84; Conservative 8; Mismatches 24; Indels 5; Gaps 1;

QY 1 EVOLVESGGGVGGGSLRLSCAAGFNIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
 DB 1 EVOLVESGGGVGGGSLRLSCAAGFTFSFGYGMHWRAQPGKLEWVAIVSYGSKNTY 60
 QY 61 ADVSKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYW-----WGQGLTVTVS 115
 DB 61 ADVSKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYW-----WGQGLTVTVS 120
 QY 116 S 116
 DB 121 S 121

RESULT 8

Q8WUJ8 PRELIMINARY; PRT; 573 AA.
 ID Q8WUJ8
 AC Q8WUJ8;

```

DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR PIR; S21205; S21205.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; PD072344033AC530 CRC64;

Query Match
Best Local Similarity 67.9%; Score 419; DB 4; Length 573;
Matches 86; Conservative 9; Mismatches 21; Indels 8; Gaps 2;

QY 1 EVOLVESGGGLVOPGSGRLSCAASGFTNIDYIMHWRAQPGKLEWVARIDPANDNTIY 60
DB 20 EVOLVESGGGLVOPGSGRLSCAASGFTNIDYIMHWRAQPGKLEWVARIDPANDNTIY 79
QY 61 ADVSKGRFTISSDSSKNTAYLQNSLRADTVAYYCT--ASGYWFAV-----WGQGTIV 112
DB 80 ADVSKGRFTISSDSSKNTAYLQNSLRADTVAYYCT--ASGYWFAV-----WGQGTIV 139
QY 113 TVSS 116
DB 140 TVSS 143

RESULT 9
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: isolation from a
human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSP; P01772; 2F84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match
Best Local Similarity 67.6%; Score 417; DB 4; Length 112;
Matches 72.3%; Pred. No. 1.4e-35;

```

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Matches 81; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSGRLSCAASGFTNIDYIMHWRAQPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGLVOPGSGRLSCAASGFTNIDYIMHWRAQPGKLEWVARIDPANDNTIY 60
QY 61 ADVSKGRFTISSDSSKNTAYLQNSLRADTVAYYCT--ASGYWFAV-----WGQGTIV 112
DB 61 ADVSKGRFTISSDSSKNTAYLQNSLRADTVAYYCT--ASGYWFAV-----WGQGTIV 112

RESULT 10
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werwe P.V., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035023; AAD56259.1; -.
DR PIR; S21205; S21205.
DR HSP; P01772; 2F84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match
Best Local Similarity 67.3%; Score 415; DB 4; Length 118;
Matches 84; Conservative 7; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGRLSCAASGFTNIDYIMHWRAQPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGLVOPGSGRLSCAASGFTNIDYIMHWRAQPGKLEWVARIDPANDNTIY 60
QY 61 ADVSKGRFTISSDSSKNTAYLQNSLRADTVAYYCT--ASGYWFAV-----WGQGTIV 115
DB 61 ADVSKGRFTISSDSSKNTAYLQNSLRADTVAYYCT--ASGYWFAV-----WGQGTIV 117

RESULT 11
Q96K68 PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Hypothetical protein FL114473.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Mammary gland;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

```

RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,
 RA Nagatsuma M., Hosori T., Kaku Y., Kodaira H., Kondo Y., Sugawara M.,
 RA Takahashi M., Chiba Y., Ichida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Iwayanagi T.,
 RA Nimomura K., Wakamatsu A., Nakamura Y., Nagahari K., Maehuo Y.,
 RT "NEDO human cDNA sequencing project."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK027379; BAB55072.1; -
 DR PIR: S21205; S21205.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00406; Ig; 1.
 DR PROSITE: PS50835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Hypothetical protein.
 KM HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 494 AA; 5308 MW; 9A1D7AB5ABE4C0E CRC64;

Query Match 67.3%; Score 415; DB 4; Length 494;
 Best Local Similarity 68.0%; Pred. No. 1.5e-34;
 Matches 83; Conservative 11; Mismatches 22; Indels 6; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDTIY 60
 DB 20 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDTIY 79
 QY 61 ADVSKGRFTISDDSKNTAVLQNMSLRAEDTAVVYCT-----ASGYFAYWGGLT 114
 DB 80 RDSVKGKFTISRDAKNSLYLQNMSLRVEDTAVVYCTGNGALICGFSPWGGTLVTV 139
 QY 115 SS 116
 DB 140 SS 141

RESULT 12

Q9UL88 PRELIMINARY; PRT; 131 AA.

AC Q9UL88;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035026; AAD56262.1; -
 DR PIR: S21205; S21205.
 DR HSSP: P01810; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR NON_TER 1
 FT 131
 SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E537DEAD0 CRC64;

Query Match 66.4%; Score 409.5; DB 4; Length 131;
 Best Local Similarity 64.9%; Pred. No. 1e-34;
 Matches 85; Conservative 6; Mismatches 25; Indels 15; Gaps 2;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPAND--NT 58
 DB 1 EVOLVESGGGLVOPGSLRLSCAASGFTFSKAMSWVRQAPGKLEWVGAIKKTGGCT 60
 QY 59 IYADVSKGRFTISDDSKNTAVLQNMSLRAEDTAVVYCT-----ASGYFAY 105
 DB 61 DYAPVKGRLTISRDSKNTLYLRMSLKTEDTAVVYCTGTITIIIVITSSKRTSFEY 120
 QY 106 WGQGLTVTVSS 116
 DB 121 WGQGLTVTVSS 131

RESULT 13

Q8NSK4 PRELIMINARY; PRT; 499 AA.

AC Q8NSK4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strauberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC032249; AAH32249.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_CL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00409; Ig; 4.
 DR SMART: SM00407; IGL1; 2.
 DR SMART: SM00406; Ig; 1.
 DR PROSITE: PS50835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 66.4%; Score 409.5; DB 4; Length 499;
 Best Local Similarity 63.8%; Pred. No. 5.6e-34;
 Matches 81; Conservative 13; Mismatches 22; Indels 11; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDTIY 60
 DB 20 EVOLVESGGGVPRPGSLRLSCATSGFTPDGASWVRQAPGKLEWVSSINNGSGTNY 79
 QY 61 ADVSKGRFTISDDSKNTAVLQNMSLRAEDTAVVYCT-----TAGYFAYWGGLT 109
 DB 80 ADVSKGRFTISRDAKNSLYLQNMSLRVEDTAVVYCTGNGALICGFSPWGGTLVTV 139
 QY 110 TVTVTVSS 116
 DB 140 TVTVTVSS 146

RESULT 14

Q91Z05 PRELIMINARY; PRT; 473 AA.

AC Q91Z05;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN A0044919.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010327; AAH10327.1; -.
 DR MGD; MGI:2144967; A0044919.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; Cytochrome_B5.
 DR InterPro; IPR007110; Iq-like.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003596; Iq_v.
 DR Pfam; PF00047; Iq; 3.
 DR SMART; SM00406; Iq; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 DR PROSITE; PS50835; Iq LIKE; 4.
 DR PROSITE; PS00290; Iq_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 65.8%; Score 406; DB 11; Length 473;
 Best Local Similarity 67.2%; Pred. No. 1.2e-33;
 Matches 80; Conservative 12; Mismatches 23; Indels 4; Gaps 2;

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGFTFSNYYHWRAQPGKLEWVARIDPANDNTIY 60
 DB 20 EVOLVESGGGLVOPGGSLRLSCAASGFTFSNYYHWRAQPGKLEWVARIDPANDNTIY 79
 QY 61 ADSVYKGRFTISDDSKNTAYLQNNSLRAEDTAVYYCTASGYWFA--YWGQGLVTVSS 116
 DB 80 ADITYKGRFTISRDKSKNTAYLQNNSLRAEDTAVYYCTASGYWFA--YWGQGLVTVSS 137

RESULT 15

Q80217 PRELIMINARY; PRT; 487 AA.
 AC 080217;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC049143; AAH49143.1; -.
 DR InterPro; IPR003599; Iq.
 DR InterPro; IPR007110; Iq-like.
 DR InterPro; IPR003597; Iq cl.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003596; Iq_v.
 DR Pfam; PF00047; Iq; 3.
 DR SMART; SM00406; Iq; 1.
 DR SMART; SM00407; Iq; 3.
 DR SMART; SM00406; Iq; 1.
 DR PROSITE; PS50835; Iq LIKE; 4.
 DR PROSITE; PS00290; Iq_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;

Query Match 65.4%; Score 403.5; DB 11; Length 487;
 Best Local Similarity 64.2%; Pred. No. 2.3e-33;
 Matches 79; Conservative 17; Mismatches 20; Indels 7; Gaps 2;

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGFTFSNYYHWRAQPGKLEWVARIDPANDNTIY 58

DB 20 EVLLEBAGGGLVOPGGSMKLSCAASGFTFSNYYHWRAQPGKLEWVARIDPANDNTIY 79
 QY 59 IYADSVYKGRFTISDDSKNTAYLQNNSLRAEDTAVYYCTASGY-----WFAWGGGLTVT 113
 DB 80 HYAESVYKGRFTISRDKSKNTAYLQNNSLRAEDTAVYYCTASGY-----WFAWGGGLTVT 139
 QY 114 VSS 116
 DB 140 VSS 142

Search completed: May 13, 2004, 17:01:47
 Job time : 131.982 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:57:28 ; Search time 48.2143 Seconds

(without alignments)
115.642 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566
Sequence: 1 DDMTQSPSSLSASVGDRTVITCRASOSISNNIHWYQKRGKAPKLLIYASOSISVPS 108

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCrus COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	496	87.6	108	3	US-08-974-899-3
2	491	86.7	107	2	US-07-934-373C-18
3	491	86.7	107	3	US-08-437-642B-18
4	491	86.7	107	4	US-08-146-206C-18
5	491	86.7	107	4	US-08-648-067A-14
6	491	86.7	107	4	US-09-705-686-18
7	491	86.7	107	5	PCT-US93-07832-18
8	491	86.7	109	2	US-07-934-373C-3
9	491	86.7	109	3	US-08-437-642B-3
10	491	86.7	109	4	US-08-146-206C-3
11	491	86.7	109	4	US-09-705-686-3
12	491	86.7	109	5	PCT-US93-07832-3
13	489	86.4	109	3	US-09-157-370-3
14	482	85.2	107	2	US-07-934-373C-17
15	482	85.2	107	3	US-08-437-642B-17
16	482	85.2	107	4	US-08-146-206C-17
17	482	85.2	107	4	US-09-705-686-17
18	482	85.2	107	5	PCT-US93-07832-17
19	482	85.2	108	2	US-08-379-057-29
20	482	85.2	109	3	US-07-934-373C-47
21	482	85.2	109	3	US-08-437-642B-47
22	482	85.2	214	2	US-07-934-373C-39
23	482	85.2	214	2	US-07-934-373C-40
24	482	85.2	214	2	US-08-788-880-11
25	482	85.2	214	3	US-08-437-642B-39
26	482	85.2	214	3	US-08-437-642B-40
27	482	85.2	214	3	US-09-097-309-2

28	482	85.2	214	3	US-09-097-171A-2	Sequence 2, Appl
29	482	85.2	214	4	US-09-460-587-2	Sequence 2, Appl
30	482	85.2	214	5	PCT-US93-07832-39	Sequence 39, Appl
31	482	85.2	214	5	PCT-US93-07832-40	Sequence 40, Appl
32	482	85.2	233	2	US-07-934-373C-25	Sequence 25, Appl
33	482	85.2	233	3	US-08-437-642B-25	Sequence 25, Appl
34	482	85.2	233	4	US-08-146-206C-25	Sequence 25, Appl
35	482	85.2	233	4	US-09-705-686-25	Sequence 25, Appl
36	482	85.2	233	5	PCT-US93-07832-25	Sequence 25, Appl
37	482	85.2	237	3	US-09-097-309-6	Sequence 6, Appl
38	482	85.2	237	3	US-09-097-171A-10	Sequence 10, Appl
39	482	85.2	237	3	US-09-422-712B-2	Sequence 2, Appl
40	482	85.2	237	3	US-09-607-756-2	Sequence 2, Appl
41	482	85.2	237	4	US-09-460-587-6	Sequence 6, Appl
42	481	85.0	108	2	US-08-378-939-32	Sequence 32, Appl
43	481	85.0	108	2	US-08-378-939-34	Sequence 34, Appl
44	481	85.0	108	4	US-09-025-769B-14	Sequence 14, Appl
45	480	84.8	111	1	US-08-137-117D-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-08-974-899-3

Sequence 3, Application US/08974899

Patent No. 6037454

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.

APPLICANT: Jardiou, Paula M.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899FILING DATE:
CLASSIFICATION: 536PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971

FILING DATE: 11/27/96

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P1014R1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-974-899-3

Query Match 87.6%; Score 496; DB 3; Length 108;
Best Local Similarity 91.7%; Pred. 1.1e-35;
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DDMTQSPSSLSASVGDRTVITCRASOSISNNIHWYQKRGKAPKLLIYASOSISVPS 60
Db 1 DDMTQSPSSLSASVGDRTVITCRASOSISNNIHWYQKRGKAPKLLIYASOSISVPS 60

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QY      61 RFGSGSGSDFTLTISLQEDFATYYCQGSNSWPYTFGGTKVEIKR 108
        |||||
Db      61 RFGSGSGSDFTLTISLQEDFATYYCQYNSLPTWTFGGTKVEIKR 108
        |||||

```

RESULT 2
US-07-934-373C-18
Sequence 18, Application US/07934373C

1 APPLICANT: Paul J. Carter
 2 APPLICANT: Leonard G. Presta
 3 TITLE OF INVENTION: Immunoglobulin Variants
 4 NUMBER OF SEQUENCES: 48
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESS: Genentech, Inc.
 7 CITY: San Francisco, CA 94608
 8 COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530

Query Match	86.7%;	Score 491;	DB 2;	Length 107;
Best Local Similarity	91.6%;	Pred. No. 2.8e-35;		
Matches 98;	Conservative	1;	Mismatches 8;	Indels 0;
				Gaps 0

Dy 61 RFGSGSGSTDTLTIISSLPEDPATYCCQNSWPYTFGGGTKEIK 107
Dd 61 RFGSGSGSTDTLTIISSLPEDPATYCCQNSLWPTIRGGGTKEIK 107

RESULT 3
US-08-437-642B-18
Sequence 18 Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc
STREET: 1 DNA way
CITY: South San Francisco
STATE: California
COUNTRY: USA

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Winpatin (Genentech)
6
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/08/437,642B
9 FILING DATE: 09-May-1995
10 CLASSIFICATION: 530
11 PRIOR APPLICATION DATA:
12

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Query Match	86.7%;	Score 491;	DB 3;	Length 107;
Best Local Similarity	91.6%;	Pred. No. 2.8e-35;		
Matches 98;	Conservative 1;	Mismatches 8;	Indels 0;	Gaps 0;

QY 61 RFGSGSGSDFTLTITSSLPEDPATYCCQOSNSWYTFGGQTKVEIK 107
| | | | | : | | | | |
Db 61 RFGSGSGSDFTLTITSSLPEDPATYCCQYNSLPWTFGGQTKVEIK 107

RESULT 4
 US-08-146-206C-18
 ; Sequence 18, Application US/08146206C
 ; Patent No. 6407213
 ; GENERAL INFORMATION:
 ; APPLICANT: Carter, Paul J.
 ; APPLICANT: Prestia, Leonard G.
 ; TITLE OF INVENTION: Method for Making Humanized Antibodies
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-18

Query Match 86.7%; Score 491; DB 4; Length 107;
Best Local Similarity 91.6%; Pred. No. 2.8e-35;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60

QY 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSWPTFGQGTKEIK 107
DB 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSLPTWFGQGTKEIK 107

RESULT 5
US-09-648-067A-14
Sequence 14, Application US/09648067A
Patent No. 6627196
GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
APPLICANT: Shak Steven
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US/09/648,067A
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 14
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match 86.7%; Score 491; DB 4; Length 107;
Best Local Similarity 91.6%; Pred. No. 2.8e-35;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60

QY 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSWPTFGQGTKEIK 107
DB 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSLPTWFGQGTKEIK 107

RESULT 6
US-09-705-686-18
Sequence 18, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-NO. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match 86.7%; Score 491; DB 4; Length 107;
Best Local Similarity 91.6%; Pred. No. 2.8e-35;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60

QY 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSWPTFGQGTKEIK 107
DB 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSLPTWFGQGTKEIK 107

RESULT 7
PCT-US93-07832-18
Sequence 18, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

Query Match 86.7%; Score 491; DB 4; Length 107;
Best Local Similarity 91.6%; Pred. No. 2.8e-35;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-18

Query Match 86.7%; Score 491; DB 5; Length 107;
Best Local Similarity 91.6%; Pred. No. 2.8e-35;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVTTTCRASQISNNLHMVQOKPKAPKLLIYASQISGVPS 60
DB 1 DIQWTQSPSSLSASVGRVTTTCRASQISNNLHMVQOKPKAPKLLIYASQISGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQSNMSPYFGGTKEIKR 107
DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQSNMSPYFGGTKEIKR 107

RESULT 8
US-07-934-373C-3
Sequence 3, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-3

Query Match 86.7%; Score 491; DB 2; Length 109;
Best Local Similarity 89.8%; Pred. No. 2.9e-35;
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVTTTCRASQISNNLHMVQOKPKAPKLLIYASQISGVPS 60
DB 1 DIQWTQSPSSLSASVGRVTTTCRASQDVSSYLAWYQOKPKAPKLLIYASQISGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQSNMSPYFGGTKEIKR 108
DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQSNMSPYFGGTKEIKR 108

RESULT 9
US-08-437-642B-3
Sequence 3, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-6428-3

Query Match 86.7%; Score 491; DB 3; Length 109;
Best Local Similarity 89.8%; Pred. No. 2.9e-35;
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTPSSISASVGVGVITTCRASOSISNNLMHYOQKPKAKPLIYHASOSISGVPS 60
1 DIQWTPSSISASVGVGVITTCRASQDVSSYLAHYOQKPKAKPLIYHASOSISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPYTFGGQTKVEIKR 108
61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSLPYTFGGQTKVEIKR 108

RESULT 10
US-08-146-206C-3
Sequence 3, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146, 206C
FILING DATE: 17-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-3

Query Match 86.7%; Score 491; DB 4; Length 109;
Best Local Similarity 89.8%; Pred. No. 2.9e-35;
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTPSSISASVGVGVITTCRASOSISNNLMHYOQKPKAKPLIYHASOSISGVPS 60
1 DIQWTPSSISASVGVGVITTCRASQDVSSYLAHYOQKPKAKPLIYHASOSISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPYTFGGQTKVEIKR 108
61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSLPYTFGGQTKVEIKR 108

Db 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSLPYTFGGQTKVEIKR 108

RESULT 11
US-09-705-686-3
Sequence 3, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705, 686
FILING DATE: 02-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-686-3

Query Match 86.7%; Score 491; DB 4; Length 109;
Best Local Similarity 89.8%; Pred. No. 2.9e-35;
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTPSSISASVGVGVITTCRASOSISNNLMHYOQKPKAKPLIYHASOSISGVPS 60
1 DIQWTPSSISASVGVGVITTCRASQDVSSYLAHYOQKPKAKPLIYHASOSISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPYTFGGQTKVEIKR 108
61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSLPYTFGGQTKVEIKR 108

RESULT 12
PCT-US93-07832-3
Sequence 3, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

```

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-3

Query Match      86.7%; Score 491; DB 5; Length 109;
Best Local Similarity 89.8%; Pred. No. 2.9e-35;
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNHLHWYQOKPKGKAPKLLIYHASQISGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNHLHWYQOKPKGKAPKLLIYHASQISGVPS 60

QY 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQNSWPTYFGQGTVEIKR 108
DB 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQNSWPTYFGQGTVEIKR 108

RESULT 13
US-09-157-370-3
Sequence 3, Application US/09157370A
Patent No. 6262238
GENERAL INFORMATION:
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P8341-8072
CURRENT APPLICATION NUMBER: US/09/157,370A
EARLIER FILING DATE: 1998-09-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER FILING DATE: 1997-01-14
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER FILING DATE: 1995-07-06
EARLIER APPLICATION NUMBER: DE/P44 25 115.7
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-157-370-3

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Query Match      86.4%; Score 489; DB 3; Length 109;
Best Local Similarity 90.7%; Pred. No. 4.3e-35;
Matches 96; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNHLHWYQOKPKGKAPKLLIYHASQISGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNHLHWYQOKPKGKAPKLLIYHASQISGVPS 60

QY 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQNSWPTYFGQGTVEIKR 108
DB 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQNSWPTYFGQGTVEIKR 108

RESULT 14
US-07-934-373C-17
Sequence 17, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO. 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-07-934-373C-17

Query Match      85.2%; Score 482; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.7e-34;
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNHLHWYQOKPKGKAPKLLIYHASQISGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNHLHWYQOKPKGKAPKLLIYHASQISGVPS 60

QY 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQNSWPTYFGQGTVEIKR 107
DB 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQNSWPTYFGQGTVEIKR 107

RESULT 15
US-08-437-642B-17

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Sequence 17, Application US/08437642B
Patent No. 6054297

GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino acid
TOPOLOGY: Linear

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:57:28 ; Search time 51.7857 Seconds
(without alignments)
115.642 Million cell updates/sec

Title: US-09-910-483-5
Perfect score: 617
Sequence: 1 EVGLVBSGGGLVQPGSLRL.....TASGYWAFYWGQTLTVVSS 116

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Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	518	84.0	120	3	US-08-437-642B-42
3	518	84.0	449	4	US-09-679-397-2
4	518	84.0	449	4	US-09-680-148-2
5	518	84.0	449	4	US-09-304-465A-2
6	518	84.0	461	2	US-08-463-587A-26
7	518	84.0	461	2	US-08-463-667A-4
8	518	84.0	461	3	US-08-923-854-26
9	518	84.0	461	5	PCT-US91-09133-27
10	510	82.7	120	2	US-07-934-373C-2
11	510	82.7	120	2	US-07-934-373C-48
12	510	82.7	120	3	US-08-437-642B-2
13	510	82.7	120	4	US-08-146-206C-2
14	510	82.7	120	4	US-09-705-686-2
15	510	82.7	120	5	PCT-US93-07832-2
16	504	81.7	120	2	US-07-934-373C-44
17	504	81.7	120	3	US-08-437-642B-44
18	471.5	76.4	119	1	US-08-053-171-12
19	468.5	75.9	467	1	US-08-704-744-81
20	462	74.9	122	2	US-07-934-373C-45
21	462	74.9	122	3	US-08-437-642B-45
22	462	74.9	122	4	US-08-146-206C-26
23	462	74.9	122	4	US-09-705-686-26
24	458	74.2	253	3	US-09-027-449-52
25	458	74.2	253	3	US-09-027-449-55
26	458	74.2	253	3	US-08-804-444A-52
27	458	74.2	253	3	US-08-804-444A-55

28	458	74.2	253	3	US-09-026-985-52	Sequence 52, Appl
29	458	74.2	253	3	US-09-026-985-55	Sequence 55, Appl
30	458	74.2	253	4	US-09-121-952A-52	Sequence 52, Appl
31	458	74.2	253	4	US-09-121-952A-55	Sequence 55, Appl
32	458	74.2	253	4	US-09-234-340A-52	Sequence 52, Appl
33	458	74.2	253	4	US-09-234-340A-55	Sequence 55, Appl
34	458	74.2	256	3	US-09-027-449-70	Sequence 70, Appl
35	458	74.2	256	3	US-09-026-985-70	Sequence 70, Appl
36	458	74.2	256	4	US-09-121-952A-70	Sequence 70, Appl
37	458	74.2	256	4	US-09-234-340A-70	Sequence 70, Appl
38	458	74.2	298	3	US-09-027-449-60	Sequence 60, Appl
39	458	74.2	298	3	US-08-804-444A-60	Sequence 60, Appl
40	458	74.2	298	3	US-09-026-985-60	Sequence 60, Appl
41	458	74.2	298	4	US-09-121-952A-60	Sequence 60, Appl
42	458	74.2	298	4	US-09-234-340A-60	Sequence 60, Appl
43	458	74.2	452	3	US-09-027-449-71	Sequence 71, Appl
44	458	74.2	452	3	US-09-026-985-71	Sequence 71, Appl
45	458	74.2	452	4	US-09-121-952A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-07-934-373C-42
Sequence 42, Application US/07934373C
Patent No. 3821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-42
Query Match 84.0%; Score 518; DB 2; Length 120;
Best Local Similarity 85.8%; Pred. No. 2.1e-42;
Matches 103; Conservative 2; Mismatches 11; Gaps 1;
QY 1 EVGLVBSGGGLVQPGSLRLSCASGNINIKDTYIHWVRQAPGKGLIEWVARIDPANDNTIY 60

Db 1 EVOLVESGGGLVOPGSLRLSCAASGFMNFKDTYIHWRQAPGKLEWVARIPDNDNTIY 60
QY 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRADTAIVYYCTASG----YMFAYWGQGLTVTVSS 116
Db 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRADTAIVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

RESULT 2

US-08-437-642B-42
; Sequence 42, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-42

Query Match 84.0%; Score 518; DB 3; Length 120;
Best Local Similarity 85.8%; Pred. No. 2.1e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFMNFKDTYIHWRQAPGKLEWVARIPDNDNTIY 60
Db 1 EVOLVESGGGLVOPGSLRLSCAASGFMNFKDTYIHWRQAPGKLEWVARIPDNDNTIY 60
QY 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRADTAIVYYCTASG----YMFAYWGQGLTVTVSS 116
Db 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRADTAIVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

RESULT 3

US-09-679-397-2
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
; APPLICANT: BASBY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D2
; CURRENT APPLICATION NUMBER: US/09/679,397
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; US-09-679-397-2

Query Match 84.0%; Score 518; DB 4; Length 449;
Best Local Similarity 85.8%; Pred. No. 9.3e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFMNFKDTYIHWRQAPGKLEWVARIPDNDNTIY 60
Db 1 EVOLVESGGGLVOPGSLRLSCAASGFMNFKDTYIHWRQAPGKLEWVARIPDNDNTIY 60
QY 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRADTAIVYYCTASG----YMFAYWGQGLTVTVSS 116
Db 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRADTAIVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

RESULT 4
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
; APPLICANT: BASBY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D1
; CURRENT APPLICATION NUMBER: US/09/680,148
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
; US-09-680-148-2

Query Match 84.0%; Score 518; DB 4; Length 449;
Best Local Similarity 85.8%; Pred. No. 9.3e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFMNFKDTYIHWRQAPGKLEWVARIPDNDNTIY 60
Db 1 EVOLVESGGGLVOPGSLRLSCAASGFMNFKDTYIHWRQAPGKLEWVARIPDNDNTIY 60
QY 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRADTAIVYYCTASG----YMFAYWGQGLTVTVSS 116
Db 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRADTAIVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

RESULT 5
US-09-304-465A-2
Sequence 2, Application US/09304465A
Patent No. 6489447
GENERAL INFORMATION:
APPLICANT: BASEY, CAROL D.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1
CURRENT APPLICATION NUMBER: US/09/304,465A
CURRENT FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 449
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized.
Patent No. 6489447
US-09-304-465A-2

Query Match 84.0%; Score 518; DB 4; Length 449;
Best Local Similarity 85.8%; Pred. No. 9.3e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFRINIKDTYIHWYRQAPGKLEWVARIDPANDTIY 60
1 EVQLVESGGGLVPGGSLRLSCAASGFRINIKDTYIHWYRQAPGKLEWVARIDPANDTIY 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFRINIKDTYIHWYRQAPGKLEWVARIDPANDTIY 60

QY 61 ADSVKGFRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 116
61 ADSVKGFRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 116
DB 61 ADSVKGFRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 120

RESULT 6
US-08-463-587A-26
Sequence 26, Application US/08463587A
Patent No. 5821047
GENERAL INFORMATION:
APPLICANT: Garrard, Lisa J.
APPLICANT: Henner, Dennis J.
APPLICANT: Bass, Steven
APPLICANT: Greene, Ronald
APPLICANT: Lowman, Henry B.
APPLICANT: Wells, James A.
APPLICANT: Matthews, David J.
TITLE OF INVENTION: ENRICHMENT METHOD FOR VARIANT PROTEINS WITH
TITLE OF INVENTION: ALTERED BINDING PROPERTIES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,587A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/050058
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09133

FILING DATE: 03-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743614
FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715300
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/683400
FILING DATE: 10-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/621667
FILING DATE: 03-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P0645PAD2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-7467
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-587A-26

Query Match 84.0%; Score 518; DB 2; Length 461;
Best Local Similarity 85.8%; Pred. No. 9.6e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFRINIKDTYIHWYRQAPGKLEWVARIDPANDTIY 60
24 EVQLVESGGGLVPGGSLRLSCAASGFRINIKDTYIHWYRQAPGKLEWVARIDPANDTIY 83
DB 24 EVQLVESGGGLVPGGSLRLSCAASGFRINIKDTYIHWYRQAPGKLEWVARIDPANDTIY 83

QY 61 ADSVKGFRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 116
84 ADSVKGFRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 143
DB 84 ADSVKGFRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 143

RESULT 7
US-08-463-667A-4
Sequence 4, Application US/08463667A
Patent No. 5834598
GENERAL INFORMATION:
APPLICANT: Garrard, Lisa J.
APPLICANT: Henner, Dennis J.
APPLICANT: Bass, Steven
APPLICANT: Greene, Ronald
APPLICANT: Lowman, Henry B.
APPLICANT: Wells, James A.
APPLICANT: Matthews, David J.
TITLE OF INVENTION: ENRICHMENT METHOD FOR VARIANT PROTEINS
TITLE OF INVENTION: WITH ALTERED BINDING PROPERTIES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: United States
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,667A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/050,058
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US91/09133
FILING DATE: 03-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,614
FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,300
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683,400
FILING DATE: 10-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,667
FILING DATE: 03-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
REGISTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER: 645PAD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 225-1249
TELEFAX: (415) 952-9881
TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-667A-4

Query Match 84.0%; Score 518; DB 2; Length 461;
Best Local Similarity 85.8%; Pred. No. 9.6e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVRQAPGKGLEWVARIDPANDNTIY 60
DB 24 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVRQAPGKGLEWVARIDPANDNTIY 83

QY 61 ADSVKGRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YFPAWGQGLTVTVSS 116
DB 84 ADSVKGRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YFPAWGQGLTVTVSS 143

RESULT 8
US-08-923-854-26
Sequence 26, Application US/08923854
Patent No. 6040136
GENERAL INFORMATION:
APPLICANT: Garrard, Lisa J.
APPLICANT: Henner, Dennis J.
APPLICANT: Baas, Steven
APPLICANT: Greene, Ronald
APPLICANT: Lowman, Henry B.
APPLICANT: Matthews, David J.
TITLE OF INVENTION: ENRICHMENT METHOD FOR VARIANT PROTEINS WITH
TITLE OF INVENTION: ALTERED BINDING PROPERTIES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463587
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: 08/050058
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09133
FILING DATE: 03-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743614
FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715300
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/683400
FILING DATE: 10-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/621667
FILING DATE: 03-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P0645PAD2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-7467
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-923-854-26

Query Match 84.0%; Score 518; DB 3; Length 461;
Best Local Similarity 85.8%; Pred. No. 9.6e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVRQAPGKGLEWVARIDPANDNTIY 60
DB 24 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVRQAPGKGLEWVARIDPANDNTIY 83

QY 61 ADSVKGRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YFPAWGQGLTVTVSS 116
DB 84 ADSVKGRFTISDSSKNTAYLQNNSLRAEDTAVYYCTASG---YFPAWGQGLTVTVSS 143

RESULT 9
PCT-US91-09133-27
Sequence 27, Application PCT/US9109133
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Garrard, Lisa J.
APPLICANT: Henner, Dennis J.
APPLICANT: Baas, Steven
APPLICANT: Greene, Ronald
APPLICANT: Lowman, Henry B.
APPLICANT: Matthews, David J.
TITLE OF INVENTION: Enrichment Method For Variant Proteins
TITLE OF INVENTION: With Altered Binding Properties
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09133
FILING DATE: 19911203
CLASSIFICATION: 425
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743614
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715300
APPLICATION NUMBER: 07/683400
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/621667
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: 645P4
TELEPHONE: 415/266-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US91-09133-27

Query Match 84.0%; Score 518; DB 5; Length 461;
Best Local Similarity 85.8%; Pred. No. 9.6e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGPNIKDTYIHWYRQAPGKLEWVARIDPANDNTIY 60
DB 24 EVOLVESGGGLVPGGSLRLSCAASGPNIKDTYIHWYRQAPGKLEWVARIYPNGYTRY 83
QY 61 ADSVKGFTISSDDSKNTAYLQWNSLRAPDTAVYYCTASG---YMFAYWGQGLTVTVSS 116
DB 84 ADSVKGFTISSDDSKNTAYLQWNSLRAPDTAVYYCTASG---YMFAYWGQGLTVTVSS 143

RESULT 10
US-07-934-373C-2
Sequence 2, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-07-934-373C-2

Query Match 82.7%; Score 510; DB 2; Length 120;
Best Local Similarity 85.0%; Pred. No. 1.2e-41;
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGPNIKDTYIHWYRQAPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGPNIKDTYIHWYRQAPGKLEWVARIYPNGYTRY 60
QY 61 ADSVKGFTISSDDSKNTAYLQWNSLRAPDTAVYYCTASG---YMFAYWGQGLTVTVSS 116
DB 61 ADSVKGFTISSDDSKNTAYLQWNSLRAPDTAVYYCTASG---YMFAYWGQGLTVTVSS 120

RESULT 11
US-07-934-373C-48
Sequence 48, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid

TOPOLOGY: Linear
US-07-934-373C-48

Query Match 82.7%; Score 510; DB 2; Length 120;
Best Local Similarity 85.0%; Pred. No. 1.2e-41;
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPDNDNTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPDNTY 60
QY 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCSRWGSDGFYANDVMGQGLTVTVSS 120

RESULT 12
US-08-437-642B-2

; Sequence 2, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-2

Query Match 82.7%; Score 510; DB 3; Length 120;

Best Local Similarity 85.0%; Pred. No. 1.2e-41;
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPDNDNTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPDNDNTY 60

DB 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPDNTY 60

QY 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCSRWGSDGFYANDVMGQGLTVTVSS 120

RESULT 13
US-08-146-206C-2

; Sequence 2, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-2

Query Match 82.7%; Score 510; DB 4; Length 120;
Best Local Similarity 85.0%; Pred. No. 1.2e-41;
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPDNDNTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPDNTY 60
QY 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCSRWGSDGFYANDVMGQGLTVTVSS 120

RESULT 14

US-09-705-686-2
; Sequence 2, Application US/09705686
; Patent No. 6639055

; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
 City: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/705,686
 FILING DATE: 02-NOV-1993
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146206
 FILING DATE: 17-NOV-1993
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P1D3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: Amino acid
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-705-686-2

Query Match 82.7%; Score 510; DB 4; Length 120;
 Best Local Similarity 85.0%; Pred. No. 1.2e-41;
 Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIMHWROAPGKLEWVARIDPANDNTIY 60
 DB 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIMHWROAPGKLEWVARIYPTNGYTRY 60

QY 61 ADSVKGRFTTSSDPSKNTAYLQNNSLRAEDTAVYYCTASG----YMFAYWGQGLTVTVSS 116
 DB 61 ADSVKGRFTTSSDPSKNTAYLQNNSLRAEDTAVYYCTASG----YMFAYWGQGLTVTVSS 120

RESULT 15
 PCT-US93-07832-2
 Sequence 2, Application PC/TUS9307832
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/07832
 FILING DATE: 19930820
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/934373
 FILING DATE: 21-AUG-1992

ATTORNEY/AGENT INFORMATION:
 NAME:
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 709P2PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE:
 TELEFAX: 415/952-9881
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

PCT-US93-07832-2

Query Match 82.7%; Score 510; DB 5; Length 120;
 Best Local Similarity 85.0%; Pred. No. 1.2e-41;
 Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

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 DB 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIMHWROAPGKLEWVARIYPTNGYTRY 60

QY 61 ADSVKGRFTTSSDPSKNTAYLQNNSLRAEDTAVYYCTASG----YMFAYWGQGLTVTVSS 116
 DB 61 ADSVKGRFTTSSDPSKNTAYLQNNSLRAEDTAVYYCTASG----YMFAYWGQGLTVTVSS 120

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 Job time : 51.7857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 17:03:18 ; Search time 171.643 Seconds

(without alignments)
175.086 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566
Sequence: 1 DQMTGSPSSLSASVGRVT.....QQSNMPTFGQTKVEIKR 108

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Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	566	100.0	108	US-09-910-483-3	Sequence 3, Appl1
2	566	100.0	108	US-09-910-483-7	Sequence 7, Appl1
3	566	100.0	108	US-09-910-483-11	Sequence 11, Appl1
4	566	100.0	108	US-09-910-483-15	Sequence 15, Appl1
5	566	100.0	108	US-09-910-483-19	Sequence 19, Appl1
6	566	100.0	108	US-09-910-483-23	Sequence 23, Appl1
7	566	100.0	108	US-09-910-483-27	Sequence 27, Appl1
8	557	98.4	108	US-09-910-483-31	Sequence 31, Appl1
9	557	98.4	108	US-09-910-483-35	Sequence 35, Appl1
10	557	98.4	108	US-09-910-483-39	Sequence 39, Appl1
11	504	89.0	105	US-10-223-880-17	Sequence 17, Appl1
12	504	89.0	105	US-10-223-880-21	Sequence 21, Appl1
13	496	87.6	108	US-09-056-1608-12	Sequence 12, Appl1
14	496	87.6	108	US-09-795-798-3	Sequence 3, Appl1
15	496	87.6	108	US-10-234-671-12	Sequence 12, Appl1

16	496	87.6	109	9	US-09-811-123-6	Sequence 6, Appl1
17	496	87.6	110	14	US-10-044-896-4	Sequence 4, Appl1
18	491	86.7	107	12	US-10-600-152-14	Sequence 14, Appl1
19	491	86.7	107	14	US-10-268-501-5	Sequence 5, Appl1
20	491	86.7	107	15	US-10-608-626-5	Sequence 2, Appl1
21	488	86.2	240	9	US-09-192-854-2	Sequence 2, Appl1
22	488	86.2	240	9	US-09-968-561A-2	Sequence 2, Appl1
23	488	86.2	240	10	US-09-968-744A-2	Sequence 2, Appl1
24	488	86.2	240	12	US-09-968-561A-2	Sequence 2, Appl1
25	487	86.0	107	10	US-09-791-153A-67	Sequence 67, Appl1
26	487	86.0	107	10	US-09-859-053-30	Sequence 30, Appl1
27	482	85.2	111	14	US-10-203-754A-56	Sequence 56, Appl1
28	482	85.2	111	14	US-10-203-754A-57	Sequence 57, Appl1
29	482	85.2	214	9	US-09-940-166A-2	Sequence 2, Appl1
30	482	85.2	214	9	US-09-811-384-11	Sequence 11, Appl1
31	482	85.2	214	12	US-10-404-286-11	Sequence 11, Appl1
32	482	85.2	237	9	US-09-940-166A-6	Sequence 6, Appl1
33	482	85.2	237	14	US-10-227-694-1	Sequence 1, Appl1
34	480	84.8	236	16	US-10-038-591-48	Sequence 48, Appl1
35	479	84.6	107	15	US-10-309-762-88	Sequence 88, Appl1
36	479	84.6	108	9	US-09-905-283-73	Sequence 73, Appl1
37	479	84.6	112	14	US-10-223-880-14	Sequence 14, Appl1
38	478	84.5	107	10	US-09-848-798-156	Sequence 156, Appl1
39	478	84.5	107	14	US-10-016-986-104	Sequence 104, Appl1
40	478	84.5	128	14	US-10-428-662-31	Sequence 31, Appl1
41	478	84.5	236	16	US-10-038-591-52	Sequence 52, Appl1
42	478	84.5	291	12	US-10-406-830-10	Sequence 10, Appl1
43	477	84.3	108	11	US-09-795-798-2	Sequence 2, Appl1
44	477	84.3	111	9	US-09-920-171-7	Sequence 7, Appl1
45	477	84.3	111	14	US-10-113-996-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-910-483-3
: Publication No. US20030035798A1
: GENERAL INFORMATION:
: APPLICANT: FANG, FANG
: APPLICANT: KOHLSTADT, LORI
: APPLICANT: RENO, JOHN
: TITLE OF INVENTION: HUMANIZED ANTIBODIES
: FILE REFERENCE: 014357/027 8772
: CURRENT APPLICATION NUMBER: US/09/910,483
: CURRENT FILING DATE: 2001-07-19
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 108
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
: OTHER INFORMATION: Peptide of Hum A
US-09-910-483-3

Query Match 100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2,2e+40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQMTGSPSSLSASVGRVTTTCRASGISNNLHWYQKKGKAPKLIYASGISVPS 60
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Db 1 DQMTGSPSSLSASVGRVTTTCRASGISNNLHWYQKKGKAPKLIYASGISVPS 60
|||
QY 61 RFSGSGGTFTLTISLQPEDPATYVYCOOSNSMPTFGQTKVEIKR 108
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Db 61 RFSGSGGTFTLTISLQPEDPATYVYCOOSNSMPTFGQTKVEIKR 108
|||

RESULT 2
US-09-910-483-7

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; Sequence 7, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-7
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Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQISNNLHWYQKPKAPKLLIYHASQSIGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQISNNLHWYQKPKAPKLLIYHASQSIGVPS 60
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QY 61 RFSGSGSGTDFTLTISLSLOPEDFATYYCOQSNMWPYTFGGGTVEIKR 108
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RESULT 3

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US-09-910-483-11
; Sequence 11, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-11
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Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQISNNLHWYQKPKAPKLLIYHASQSIGVPS 60
```

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DB 61 RFSGSGSGTDFTLTISLSLOPEDFATYYCOQSNMWPYTFGGGTVEIKR 108
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RESULT 4
US-09-910-483-15
; Sequence 15, Application US/09910483
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; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-15
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Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQISNNLHWYQKPKAPKLLIYHASQSIGVPS 60
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QY 61 RFSGSGSGTDFTLTISLSLOPEDFATYYCOQSNMWPYTFGGGTVEIKR 108
DB 61 RFSGSGSGTDFTLTISLSLOPEDFATYYCOQSNMWPYTFGGGTVEIKR 108
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RESULT 5

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US-09-910-483-19
; Sequence 19, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-19
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Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQISNNLHWYQKPKAPKLLIYHASQSIGVPS 60
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DB 61 RFSGSGSGTDFTLTISLSLOPEDFATYYCOQSNMWPYTFGGGTVEIKR 108
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RESULT 6
US-09-910-483-23
; Sequence 23, Application US/09910483
; Publication No. US20030035798A1
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/ GENERAL INFORMATION:
/ APPLICANT: FANG, FANG
/ APPLICANT: KOHLSTADT, LORI
/ APPLICANT: RENO, JOHN
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
/ FILE REFERENCE: 014357/027 8772
/ CURRENT APPLICATION NUMBER: US/09/910,483
/ CURRENT FILING DATE: 2001-07-19
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
/ OTHER INFORMATION: peptide of Hum F
US-09-910-483-23
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Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DIQWTSPPSSLSASVGDVVTITCRASQISNNLHMWQOKPKAPKLLIYHASQISGVPS 60
DB 1 DIQWTSPPSSLSASVGDVVTITCRASQISNNLHMWQOKPKAPKLLIYHASQISGVPS 60
QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQGSNSWPYTFGGCTKVEIKR 108
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCQGSNSWPYTFGGCTKVEIKR 108
```

```
RESULT 7
US-09-910-483-44
/ Sequence 44, Application US/09910483
/ Publication No. US20030035798A1
/ GENERAL INFORMATION:
/ APPLICANT: FANG, FANG
/ APPLICANT: KOHLSTADT, LORI
/ APPLICANT: RENO, JOHN
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
/ FILE REFERENCE: 014357/027 8772
/ CURRENT APPLICATION NUMBER: US/09/910,483
/ CURRENT FILING DATE: 2001-07-19
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 44
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Humanized I16
/ OTHER INFORMATION: (HumI9) VH domain consensus sequence of light chain K
/ OTHER INFORMATION: Subgroup I (HumKI)
US-09-910-483-44
```

```
Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DIQWTSPPSSLSASVGDVVTITCRASQISNNLHMWQOKPKAPKLLIYHASQISGVPS 60
DB 1 DIQWTSPPSSLSASVGDVVTITCRASQISNNLHMWQOKPKAPKLLIYHASQISGVPS 60
QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQGSNSWPYTFGGCTKVEIKR 108
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCQGSNSWPYTFGGCTKVEIKR 108
```

```
RESULT 8
US-09-910-483-27
/ Sequence 27, Application US/09910483
/ Publication No. US20030035798A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: FANG, FANG
/ APPLICANT: KOHLSTADT, LORI
/ APPLICANT: RENO, JOHN
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
/ FILE REFERENCE: 014357/027 8772
/ CURRENT APPLICATION NUMBER: US/09/910,483
/ CURRENT FILING DATE: 2001-07-19
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
/ OTHER INFORMATION: peptide of Hum G
US-09-910-483-27
```

```
Query Match          98.4%; Score 557; DB 10; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.3e-39;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 DIQWTSPPSSLSASVGDVVTITCRASQISNNLHMWQOKPKAPKLLIYHASQISGVPS 60
DB 1 DIQWTSPPSSLSASVGDVVTITCRASQISNNLHMWQOKPKAPKLLIYHASQISGVPS 60
QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQGSNSWPYTFGGCTKVEIKR 108
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCQGSNSWPYTFGGCTKVEIKR 108
```

```
RESULT 9
US-09-910-483-31
/ Sequence 31, Application US/09910483
/ Publication No. US20030035798A1
/ GENERAL INFORMATION:
/ APPLICANT: FANG, FANG
/ APPLICANT: KOHLSTADT, LORI
/ APPLICANT: RENO, JOHN
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
/ FILE REFERENCE: 014357/027 8772
/ CURRENT APPLICATION NUMBER: US/09/910,483
/ CURRENT FILING DATE: 2001-07-19
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 31
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
/ OTHER INFORMATION: peptide of Hum H
US-09-910-483-31
```

```
Query Match          98.4%; Score 557; DB 10; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.3e-39;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 DIQWTSPPSSLSASVGDVVTITCRASQISNNLHMWQOKPKAPKLLIYHASQISGVPS 60
DB 1 DIQWTSPPSSLSASVGDVVTITCRASQISNNLHMWQOKPKAPKLLIYHASQISGVPS 60
QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQGSNSWPYTFGGCTKVEIKR 108
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCQGSNSWPYTFGGCTKVEIKR 108
```

```
RESULT 10
US-09-910-483-35
/ Sequence 35, Application US/09910483
/ Publication No. US20030035798A1
/ GENERAL INFORMATION:
```

```

; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 35
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-35

```

```

Query Match      98.4%; Score 557; DB 10; Length 108;
Best Local Similarity 99.1%; Pred. No. 1,3e-39;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DIOMTQSPSSLSASVGRVITTCRASQSIENNLMHWYQOKRGAAPKLLIYHASQISIGVPS 60
DB 1 DIOMTQSPSSLSASVGRVITTCRASQSIENNLMHWYQOKRGAAPKLLIYHASQISIGVPS 60
QY 61 RFGSGSGGTDFTLTITSSLOPEDFATYYCCQSNMWPYTFGQGTKEIR 108
DB 61 RFGSGSGGTDFTLTITSSLOPEDFATYYCCQSNMWPYTFGQGTKEIR 108

```

```

RESULT 11
US-10-223-880-17
; Sequence 17, Application US/10223880
; Publication No. US20030152571A1
; GENERAL INFORMATION:
; APPLICANT: JONAK, ZDENKA
; APPLICANT: JOHANSON, KYUNG O.
; APPLICANT: TAYLOR, ALEXANDER
; TITLE OF INVENTION: ANTI-ALPHA BETA 3 HUMANIZED MONOCLONAL
; FILE REFERENCE: P50629C1
; CURRENT APPLICATION NUMBER: US/10/223,880
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: wherein the sequences represent the DNA and amino
; OTHER INFORMATION: acid sequences of the Jk gene and its gene
; OTHER INFORMATION: product.
US-10-223-880-17

```

```

Query Match      89.0%; Score 504; DB 14; Length 105;
Best Local Similarity 90.5%; Pred. No. 3.5e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 DIOMTQSPSSLSASVGRVITTCRASQSIENNLMHWYQOKRGAAPKLLIYHASQISIGVPS 60
DB 1 DIOMTQSPSSLSASVGRVITTCRASQSIENNLMHWYQOKRGAAPKLLIYHASQISIGVPS 60
QY 61 RFGSGSGGTDFTLTITSSLOPEDFATYYCCQSNMWPYTFGQGTKEIR 105
DB 61 RFGSGSGGTDFTLTITSSLOPEDFATYYCCQSNMWPYTFGQGTKEIR 105

```

```

RESULT 12
US-10-223-880-21
; Sequence 21, Application US/10223880
; Publication No. US20030152571A1
; GENERAL INFORMATION:
; APPLICANT: JONAK, ZDENKA
; APPLICANT: JOHANSON, KYUNG O.
; APPLICANT: TAYLOR, ALEXANDER
; TITLE OF INVENTION: ANTI-ALPHA BETA 3 HUMANIZED MONOCLONAL
; FILE REFERENCE: P50629C1
; CURRENT APPLICATION NUMBER: US/10/223,880
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Represents an amino acid sequence of the synthetic
; OTHER INFORMATION: kappa chain based on a modified human REI kappa
; OTHER INFORMATION: chain framework
US-10-223-880-21

```

```

Query Match      89.0%; Score 504; DB 14; Length 105;
Best Local Similarity 90.5%; Pred. No. 3.5e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 DIOMTQSPSSLSASVGRVITTCRASQSIENNLMHWYQOKRGAAPKLLIYHASQISIGVPS 60
DB 1 DIOMTQSPSSLSASVGRVITTCRASQSIENNLMHWYQOKRGAAPKLLIYHASQISIGVPS 60
QY 61 RFGSGSGGTDFTLTITSSLOPEDFATYYCCQSNMWPYTFGQGTKEIR 105
DB 61 RFGSGSGGTDFTLTITSSLOPEDFATYYCCQSNMWPYTFGQGTKEIR 105

```

```

RESULT 13
US-09-056-160B-12
; Sequence 12, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998

```

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-056-160B-12
Query Match 87.6%; Score 496; DB 9; Length 108;
Best Local Similarity 91.7%; Pred. No. 1,7e-34;
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMWYQKPKKLIYASQISGVPS 60
DB 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMWYQKPKKLIYASQISGVPS 60
QY 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108
DB 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108

RESULT 14

US-09-795-798-3
Sequence 3, Application US/09795798
Publication No. US2003020736A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P101ARI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-795-798-3

Query Match 87.6%; Score 496; DB 11; Length 108;
Best Local Similarity 91.7%; Pred. No. 1,7e-34;
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMWYQKPKKLIYASQISGVPS 60
DB 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMWYQKPKKLIYASQISGVPS 60
QY 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108
DB 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108

RESULT 15

US-10-234-671-12
Sequence 12, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-234-671-12
Query Match 87.6%; Score 496; DB 14; Length 108;
Best Local Similarity 91.7%; Pred. No. 1,7e-34;
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMWYQKPKKLIYASQISGVPS 60
DB 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMWYQKPKKLIYASQISGVPS 60
QY 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108

Fri May 14 07:50:48 2004

us-09-910-483-7.may11.rapb

Page 6

Db 61 RFGSGSGSTDFTLTIFISLQPEDFATYYCQYNSLPLWTFQGTKEIKR 108

Search completed: May 13, 2004, 17:34:31
Job time : 172.143 secs

GenCore version 5.1.6
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OM:protein - protein search, using sw model

Run on: May 13, 2004, 17:03:18 ; Search time 184.357 Seconds
(without alignments)
175.086 Million cell updates/sec

Title: US-09-910-483-5

Perfect score: 617
Sequence: 1 EVOLVESGGGLVQPGSLRL.....TASGYWPAWMGQGLTVTVSS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	617	100.0	116	10	US-09-910-483-5	Sequence 5, Appl1
2	617	100.0	116	10	US-09-910-483-43	Sequence 43, Appl1
3	613	99.4	116	10	US-09-910-483-13	Sequence 13, Appl1
4	611	99.0	116	10	US-09-910-483-1	Sequence 1, Appl1
5	610	98.9	116	10	US-09-910-483-21	Sequence 21, Appl1
6	610	98.9	116	10	US-09-910-483-25	Sequence 25, Appl1
7	609	98.7	116	10	US-09-910-483-9	Sequence 9, Appl1
8	589	95.5	116	10	US-09-910-483-17	Sequence 17, Appl1
9	589	95.5	116	10	US-09-910-483-29	Sequence 29, Appl1
10	576	93.4	116	10	US-09-910-483-33	Sequence 33, Appl1
11	518	84.0	120	9	US-09-971-543-11	Sequence 11, Appl1
12	518	84.0	120	12	US-10-411-037-36	Sequence 36, Appl1
13	518	84.0	120	12	US-10-411-026-36	Sequence 36, Appl1
14	518	84.0	120	15	US-10-410-894-2	Sequence 2, Appl1
15	518	84.0	120	16	US-10-410-962-36	Sequence 36, Appl1

16	518	84.0	120	16	US-10-411-049-36	Sequence 36, Appl1
17	518	84.0	228	12	US-10-364-953-14	Sequence 14, Appl1
18	518	84.0	252	9	US-09-971-543-1	Sequence 1, Appl1
19	518	84.0	449	14	US-10-253-366-2	Sequence 2, Appl1
20	518	84.0	449	14	US-10-316-694-2	Sequence 2, Appl1
21	518	84.0	449	14	US-10-356-974-2	Sequence 2, Appl1
22	518	84.0	449	15	US-10-423-299-2	Sequence 2, Appl1
23	518	84.0	449	16	US-10-659-825-2	Sequence 2, Appl1
24	518	84.0	527	12	US-10-182-975-25	Sequence 25, Appl1
25	518	84.0	763	15	US-10-418-836-13	Sequence 13, Appl1
26	518	84.0	979	15	US-10-418-836-16	Sequence 10, Appl1
27	518	84.0	979	15	US-10-418-836-16	Sequence 16, Appl1
28	480	77.8	116	10	US-09-910-483-37	Sequence 37, Appl1
29	480	77.8	116	10	US-09-910-483-41	Sequence 41, Appl1
30	471.5	76.4	117	10	US-09-802-083-2	Sequence 2, Appl1
31	471.5	76.4	117	14	US-10-165-732A-2	Sequence 2, Appl1
32	471.5	76.4	117	14	US-10-172-785-2	Sequence 2, Appl1
33	471.5	76.4	225	12	US-10-364-953-12	Sequence 12, Appl1
34	471.5	76.4	470	14	US-10-020-786-9	Sequence 9, Appl1
35	471.5	76.4	470	14	US-10-327-694-5	Sequence 5, Appl1
36	464.5	75.3	291	12	US-10-406-830-1	Sequence 1, Appl1
37	464.5	75.3	291	12	US-10-406-830-2	Sequence 2, Appl1
38	459.5	74.5	248	10	US-09-880-748-1421	Sequence 1421, Ap
39	459.5	74.5	248	12	US-10-293-418-1421	Sequence 1421, Ap
40	458.5	74.3	119	14	US-10-073-644C-2	Sequence 2, Appl1
41	458	74.2	253	10	US-09-726-258-52	Sequence 52, Appl1
42	458	74.2	253	10	US-09-726-258-55	Sequence 55, Appl1
43	458	74.2	256	10	US-09-726-258-70	Sequence 70, Appl1
44	458	74.2	298	10	US-09-726-258-60	Sequence 60, Appl1
45	458	74.2	452	10	US-09-726-258-71	Sequence 71, Appl1

ALIGNMENTS

RESULT 1
US-09-910-483-5
; Sequence 5, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT FILING DATE: US/09/910.483
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: peptide of Hum B
US-09-910-483-5

Query Match 100.0%; Score 617; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.9e-52;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGSLRLSCAASGNIKDTYHWVRQAPGKLEWVARIDPANDTYY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGNIKDTYHWVRQAPGKLEWVARIDPANDTYY 60
QY 61 ADSYKGRFTTSDSKNTAYIQMNSLAEDTAVYYCTASGYWPAWMGQGLTVTVSS 116
DB 61 ADSYKGRFTTSDSKNTAYIQMNSLAEDTAVYYCTASGYWPAWMGQGLTVTVSS 116
RESULT 2
US-09-910-483-43

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; Sequence 43, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized 1A6
; OTHER INFORMATION: (Hum19) VH Domain consensus sequence of Heavy Chain
; OTHER INFORMATION: Subgroup III (Hum111)
US-09-910-483-43
```

```
Query Match          100.0%; Score 617; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.9e-52;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLHWARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLHWARIDPANDNTIY 60
QY 61 ADSVKGRFTTSSDSDSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTTSSDSDSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
```

```
RESULT 3
US-09-910-483-13
```

```
; Sequence 13, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: Peptide of Hum D
US-09-910-483-13
```

```
Query Match          99.4%; Score 613; DB 10; Length 116;
Best Local Similarity 99.1%; Pred. No. 1.2e-51;
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLHWARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLHWARIDPANDNTIY 60
QY 61 ADSVKGRFTTSSDSDSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTTSSDSDSKNTAVYLQMSLRAEDTAVYYCTTSGYFAYWGQGLTVTVSS 116
```

```
RESULT 4
US-09-910-483-1
```

```
; Sequence 1, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: Peptide of Hum A
US-09-910-483-1
```

```
Query Match          99.0%; Score 611; DB 10; Length 116;
Best Local Similarity 99.1%; Pred. No. 1.9e-51;
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLHWARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLHWARIDPANDNTIY 60
QY 61 ADSVKGRFTTSSDSDSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTTSSDSDSKNTAVYLQMSLRAEDTAVYYCTDSGYFAYWGQGLTVTVSS 116
```

```
RESULT 5
```

```
US-09-910-483-21
; Sequence 21, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: Peptide of Hum F
US-09-910-483-21
```

```
Query Match          98.9%; Score 610; DB 10; Length 116;
Best Local Similarity 98.3%; Pred. No. 2.3e-51;
Matches 114; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLHWARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLHWARIDPANDNTIY 60
QY 61 ADSVKGRFTTSSDSDSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTTSSDSDSKNTAVYLQMSLRAEDTAVYYCTTSGYFAYWGQGLTVTVSS 116
```

```
RESULT 6
US-09-910-483-25
; Sequence 25, Application US/09910483
```

Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: peptide of Hum G
US-09-910-483-25

Query Match 98.9%; Score 610; DB 10; Length 116;
Best Local Similarity 98.3%; Pred. No. 2.3e-51;
Matches 114; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60
QY 61 ADSVKGRTTISDDSKNTAYLQNMNLSRAEDTAVYYCTASGYWFAWVGQGLVTVSS 116
DB 61 ADSVKGRTTISADDSKNTAYLQNMNLSRAEDTAVYYCTTSGYWFAYWGQGLVTVSS 116

RESULT 7
US-09-910-483-9
; Sequence 9, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: peptide of Hum C
US-09-910-483-9

Query Match 98.7%; Score 609; DB 10; Length 116;
Best Local Similarity 98.3%; Pred. No. 2.9e-51;
Matches 114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60
QY 61 ADSVKGRTTISDDSKNTAYLQNMNLSRAEDTAVYYCTASGYWFAWVGQGLVTVSS 116
DB 61 ADSVKGRTTISDDSKNTAYLQNMNLSRAEDTAVYYCTTSGYWFAYWGQGLVTVSS 116

RESULT 8
US-09-910-483-17
; Sequence 17, Application US/09910483
; Publication No. US20030035798A1

GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: peptide of Hum E
US-09-910-483-17

Query Match 95.5%; Score 589; DB 10; Length 116;
Best Local Similarity 94.8%; Pred. No. 2.5e-49;
Matches 110; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60
QY 61 ADSVKGRTTISDDSKNTAYLQNMNLSRAEDTAVYYCTASGYWFAWVGQGLVTVSS 116
DB 61 DPKVQGRFTISADDSKNTAYLQNMNLSRAEDTAVYYCTTSGYWFAYWGQGLVTVSS 116

RESULT 9
US-09-910-483-29
; Sequence 29, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: peptide of Hum H
US-09-910-483-29

Query Match 95.5%; Score 589; DB 10; Length 116;
Best Local Similarity 94.8%; Pred. No. 2.5e-49;
Matches 110; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60
QY 61 ADSVKGRTTISDDSKNTAYLQNMNLSRAEDTAVYYCTASGYWFAWVGQGLVTVSS 116
DB 61 DPKVQGRFTISADDSKNTAYLQNMNLSRAEDTAVYYCTTSGYWFAYWGQGLVTVSS 116

RESULT 10
US-09-910-483-33
; Sequence 33, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:

APPLICANT: FANG, FANG
APPLICANT: KOHLSTADT, LORI
APPLICANT: RENO, JOHN
TITLE OF INVENTION: HUMANIZED ANTIBODIES
FILE REFERENCE: 014357/027 8772
CURRENT APPLICATION NUMBER: US/09/910,483
CURRENT FILING DATE: 2001-07-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Synthetic VH Domain
OTHER INFORMATION: peptide of Hum I
US-09-910-483-33

Query Match 93.4%; Score 576; DB 10; Length 116;
Best Local Similarity 92.2%; Pred. No. 4.4e-49;
Matches 107; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
QY 61 ADSVKGRTTISDSDSKNTAYLQMSLRADPTAVYYCTASGTPWYWGQGLTVTVSS 116
DB 61 DPKVQGRFTTISADTSKNTAYLQMSLRADPTAVYYCTTSGTWFGWGGTLTVTVSS 116

RESULT 11

US-09-971-543-11
Sequence 11, Application US/09971543
Patent No. US20020146846A1
GENERAL INFORMATION:

APPLICANT: PLUCKTUN, ANDREAS
APPLICANT: HONEGGER, ANNEMARIE
APPLICANT: WILHOLD, JORG
TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHIMERIC
TITLE OF INVENTION: IMMUNOGLOBULIN OR IMMUNOGLOBULIN FRAGMENTS, AND
FILE REFERENCE: PLUCK-3 CON
CURRENT APPLICATION NUMBER: US/09/971,543
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: PCT/EP00/03176
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: EP 99 10 7030.1
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Synthetic 4ds peptide
OTHER INFORMATION: Description of Artificial Sequence: Synthetic 4ds peptide
US-09-971-543-11

Query Match 84.0%; Score 518; DB 9; Length 120;
Best Local Similarity 85.8%; Pred. No. 1.8e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
QY 61 ADSVKGRTTISDSDSKNTAYLQMSLRADPTAVYYCTASGTPWYWGQGLTVTVSS 116
DB 61 ADSVKGRTTISADTSKNTAYLQMSLRADPTAVYYCTSRMGDGFYANDYWGQGLTVTVSS 120

RESULT 12

US-10-411-037-36
Sequence 36, Application US/10411037
Publication No. US20040043446A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
FILE REFERENCE: 040853-01-5082
CURRENT APPLICATION NUMBER: US/10/411,037
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
LENGTH: 120
TYPE: PRT
ORGANISM: Mus musculus
US-10-411-037-36

Query Match 84.0%; Score 518; DB 12; Length 120;
Best Local Similarity 85.8%; Pred. No. 1.8e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
QY 61 ADSVKGRTTISDSDSKNTAYLQMSLRADPTAVYYCTASGTPWYWGQGLTVTVSS 116
DB 61 ADSVKGRTTISADTSKNTAYLQMSLRADPTAVYYCTSRMGDGFYANDYWGQGLTVTVSS 120

RESULT 13

US-10-411-026-36
Sequence 36, Application US/10411026
Publication No. US20040063911A1
GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
FILE REFERENCE: 040853-01-5053
CURRENT APPLICATION NUMBER: US/10/411,026
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
LENGTH: 120
TYPE: PRT
ORGANISM: Mus musculus
US-10-411-026-36

Query Match 84.0%; Score 518; DB 12; Length 120;
Best Local Similarity 85.8%; Pred. No. 1.8e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVROAPGKLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVROAPGKLEWVARIPYPTNGYTRY 60
QY 61 ADSVKGRTTSSDSSKNTAYIQNNSLRAEDTAVYYCTASG---YWFAYMGQGLTVTVSS 116
DB 61 ADSVKGRTTISADTSKNTAYIQNNSLRAEDTAVYYCSRWDGDFYAMDYMGQGLTVTVSS 120

RESULT 14
US-10-410-894-2
Sequence 2, Application US/10410894
Publication No. US20030228663A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: LOWMAN, Henry B.
APPLICANT: GERSTNER, Reel B.
APPLICANT: CARTER, Paul J.
TITLE OF INVENTION: ANTI-HER2 ANTIBODY VARIANTS
FILE REFERENCE: 39766-0108 US
CURRENT APPLICATION NUMBER: US/10/410,894
CURRENT FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: homo sapiens
US-10-410-894-2

Query Match 84.0%; Score 518; DB 15; Length 120;
Best Local Similarity 85.8%; Pred. No. 1.8e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVROAPGKLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVROAPGKLEWVARIPYPTNGYTRY 60
QY 61 ADSVKGRTTSSDSSKNTAYIQNNSLRAEDTAVYYCTASG---YWFAYMGQGLTVTVSS 116
DB 61 ADSVKGRTTISADTSKNTAYIQNNSLRAEDTAVYYCSRWDGDFYAMDYMGQGLTVTVSS 120

RESULT 15
US-10-410-962-36
Sequence 36, Application US/10410962
Publication No. US2004007836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Deftrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David

APPLICANT: Chen, Xi
APPLICANT: Bove, Caryn
TITLE OF INVENTION: GLYCOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
FILE REFERENCE: 040853-01-5054
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
LENGTH: 120
TYPE: PRT
ORGANISM: Mus musculus
US-10-410-962-36

Query Match 84.0%; Score 518; DB 16; Length 120;
Best Local Similarity 85.8%; Pred. No. 1.8e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVROAPGKLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVROAPGKLEWVARIPYPTNGYTRY 60
QY 61 ADSVKGRTTSSDSSKNTAYIQNNSLRAEDTAVYYCTASG---YWFAYMGQGLTVTVSS 116
DB 61 ADSVKGRTTISADTSKNTAYIQNNSLRAEDTAVYYCSRWDGDFYAMDYMGQGLTVTVSS 120

Search completed: May 13, 2004, 17:34:31
Job time : 190.857 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:43:32 ; Search time 21.2143 Seconds
(without alignments)
265.084 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSSNSWPTFGQSTKVEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	82.2	108	KV1V_HUMAN	P04430 homo sapien
2	463	81.8	108	KV1H_HUMAN	P01600 homo sapien
3	461	81.4	108	KV1G_HUMAN	P01599 homo sapien
4	460	81.3	108	KV1R_HUMAN	P01605 homo sapien
5	458	80.9	108	KV1R_HUMAN	P01610 homo sapien
6	457	80.7	129	KV1W_HUMAN	P04431 homo sapien
7	450	79.5	108	KV1B_HUMAN	P01594 homo sapien
8	448	79.2	108	KV1E_HUMAN	P01597 homo sapien
9	446	78.8	108	KV1E_HUMAN	P01607 homo sapien
10	444	78.4	108	KV1N_HUMAN	P01606 homo sapien
11	442	78.1	108	KV1S_HUMAN	P01608 homo sapien
12	442	78.1	108	KV1S_HUMAN	P01611 homo sapien
13	441	77.9	108	KV1F_HUMAN	P01598 homo sapien
14	440	77.7	108	KV1I_HUMAN	P01604 homo sapien
15	439.5	77.7	107	KV1D_HUMAN	P01596 homo sapien
16	438	77.4	108	KV1C_HUMAN	P01595 homo sapien
17	438	77.4	108	KV1Y_HUMAN	P03662 homo sapien
18	429	75.8	108	KV1A_HUMAN	P01593 homo sapien
19	427	75.4	108	KV1X_HUMAN	P01603 homo sapien
20	426	75.3	108	KV1Q_HUMAN	P01609 homo sapien
21	422	74.6	129	KV1X_HUMAN	P04432 homo sapien
22	419.5	74.1	129	KV3H_HUMAN	P04207 homo sapien
23	416.5	73.6	109	KV1T_HUMAN	P01612 homo sapien
24	414	73.1	117	KV1J_HUMAN	P01602 homo sapien
25	408	72.1	108	KV5K_MOUSE	P01644 mus musculu
26	407	71.9	117	KV1I_HUMAN	P01624 mus musculu
27	405.5	71.6	109	KV3F_HUMAN	P01624 mus sapien
28	403	71.2	108	KV5L_MOUSE	P01645 mus musculu
29	403	71.2	108	KV5Q_MOUSE	P01648 mus musculu
30	402.5	71.1	109	KV3D_HUMAN	P01622 homo sapien
31	399.5	70.6	109	KV3B_HUMAN	P01620 homo sapien
32	399	70.5	108	KV3S_MOUSE	P01652 mus musculu
33	398.5	70.4	129	KV3M_HUMAN	P18136 homo sapien

34	398	70.3	108	KV5J_MOUSE	P01643 mus musculu
35	398	70.3	108	KV5M_MOUSE	P01646 mus musculu
36	398	70.3	108	KV5P_MOUSE	P01649 mus musculu
37	397.5	70.2	129	KV3I_HUMAN	P18135 homo sapien
38	396	70.0	108	KV5N_MOUSE	P01647 mus musculu
39	396	70.0	108	KV5Q_MOUSE	P01650 mus musculu
40	395	69.8	114	KV4A_HUMAN	P01625 homo sapien
41	395	69.8	134	KV4C_HUMAN	P06314 homo sapien
42	392	69.3	108	KV5T_MOUSE	P01653 mus musculu
43	391.5	69.2	109	KV3E_HUMAN	P01623 mus sapien
44	390	68.9	108	KV5D_MOUSE	P01636 mus musculu
45	388	68.6	108	KV5U_MOUSE	P04946 mus musculu

ALIGNMENTS

RESULT 1	ALIGNMENTS
KV1V_HUMAN	
ID KV1V_HUMAN	STANDARD; PRT; 108 AA.
AC P04430;	
DT 13-AUG-1987 (Rel. 05, Created)	
DT 13-AUG-1987 (Rel. 05, Last sequence update)	
DT 15-JUL-1999 (Rel. 38, Last annotation update)	
DE Ig kappa chain V-I region BAN.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_Taxid=9606;	
RX MEDLINE=66174817; PubMed=3083240;	
RA Dwolet P.E., O'Connor T.P., Benson M.D. ;	
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";	
RL Mol. Immunol. 23:73-78(1986).	
DR PIR; A01878; KIHUEN.	
DR HSSP; P80362; 1WTL.	
DR GO; GO:0005576; C:extracellular; NAS.	
DR GO; GO:0003823; P:antigen binding; NAS.	
DR GO; GO:0006955; P:immune response; NAS.	
DR InterPro; IPR007110; Ig_V-like.	
DR InterPro; IPR003596; Ig_V.	
DR Pfam; PF00047; Ig_V.	
DR SMART; SM00406; IGV; 1.	
DR PROSITE; PSS0835; IG_LIKE; 1.	
KW Immunoglobulin V region; Amyloid.	
FT DOMAIN 1 23	FRAMEWORK-1.
FT DOMAIN 24 34	COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49	FRAMEWORK-2.
FT DOMAIN 50 56	COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 86	FRAMEWORK-3.
FT DOMAIN 89 97	COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88	FRAMEWORK-4.
FT NON TER 108	BY SIMILARITY.
SO SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;	
Query Match 82.2%; Score 465; DB 1; Length 108;	
Best Local Similarity 83.3%; Pred. No. 8,7e-41;	
Matches 90; Conservative 7; Mismatches 11; Indels 0; Gaps 0;	
QY 1 DIQMTQSPSSLSASVGRVTTCRASQISNNLHWQKGRKPKLIYASQISGVPS 60	
DB 1 DIQMTQSPSSLSASVGRVTTCRASQISNNLHWQKGRKPKLIYASQISGVPS 60	
QY 61 RFSSGGSGTDFTLTSSLOPEDFATVYCCQSNWPTFGQSTKVEIKR 108	
DB 61 RFSSGGSGTDFTLTSSLOPEDFATVYCCQSNWPTFGQSTKVEIKR 108	
RESULT 2	
KV1H_HUMAN	STANDARD; PRT; 108 AA.
ID KV1H_HUMAN	

AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Metanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups."
 RT Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.
 DR HSSP; P80362; IWTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;
 Query Match 81.8%; Score 463; DB 1; Length 108;
 Best Local Similarity 85.2%; Pred. No. 1,4e-40;
 Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQMTSPSSLSASVGDRTVITTCRASQISNNIMHWYQKRGKAPKLLIYASQISGVPS 60
 DB 1 DIQMTSPSSLSASVGDRTVITTCRASQISNNIMHWYQKRGKAPKLLIYASQISGVPS 60
 QY 61 RFGSGSGGTDFTLTISLQPEDPATYTCQNSNMPYFGGTVEIKR 108
 DB 61 RFGSGSGGTDFTLTISLQPEDPATYTCQNSNMPYFGGTVEIKR 108
 RESULT 3
 KVIG HUMAN STANDARD; PRT; 108 AA.
 AC P01599;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Gal.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059122; PubMed=4215718;
 RA Laure C.J., Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), I. The amino acid sequence of the L-chain of kappa-type, subgroup I.";

RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
 DR PIR; A01867; KIHUCL.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600F73 CRC64;
 Query Match 81.4%; Score 461; DB 1; Length 108;
 Best Local Similarity 84.3%; Pred. No. 2,2e-40;
 Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIQMTSPSSLSASVGDRTVITTCRASQISNNIMHWYQKRGKAPKLLIYASQISGVPS 60
 DB 1 DIQMTSPSSLSASVGDRTVITTCRASQISNNIMHWYQKRGKAPKLLIYASQISGVPS 60
 QY 61 RFGSGSGGTDFTLTISLQPEDPATYTCQNSNMPYFGGTVEIKR 108
 DB 61 RFGSGSGGTDFTLTISLQPEDPATYTCQNSNMPYFGGTVEIKR 108
 RESULT 4
 KVIM HUMAN STANDARD; PRT; 108 AA.
 AC P01605;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Lay.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77038198; PubMed=824717;
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities."
 RT Scand. J. Immunol. 5:677-684 (1976).
 CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-IT1 KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
 DR PIR; A01871; KIHUXY.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.

DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;
Query Match 81.3%; Score 460; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 2.8e-40;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
Db 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGGCTKVEIKR 108
QY 1 DIQWTPSSLSASVGVGRVITTCRASQISNNLHMVYQKRGKAPKLIYASQISGVPS 60
1 DIQWTPSSLSASVGVGRVITTCRASQISNNLHMVYQKRGKAPKLIYASQISGVPS 60
Db 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGGCTKVEIKR 108
QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGGCTKVEIKR 108
Db 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGGCTKVEIKR 108
RESULT 5
KVIR_HUMAN STANDARD; PRT; 108 AA.
ID KVIR_HUMAN
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IGM
RT (proteome WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC AGAINT 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHUMK.
DR HSSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249861F0945618C CRC64;
Query Match 80.9%; Score 458; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 4.5e-40;

Matches 89; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 1 DIQWTPSSLSASVGVGRVITTCRASQISNNLHMVYQKRGKAPKLIYASQISGVPS 60
1 DIQWTPSSLSASVGVGRVITTCRASQISNNLHMVYQKRGKAPKLIYASQISGVPS 60
Db 1 DIQWTPSSLSASVGVGRVITTCRASQISNNLHMVYQKRGKAPKLIYASQISGVPS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGGCTKVEIKR 108
1 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGGCTKVEIKR 108
Db 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGGCTKVEIKR 108
RESULT 6
KVIR_HUMAN STANDARD; PRT; 129 AA.
ID KVIR_HUMAN
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X00965; CA25477.1; ALT_TERM.
DR PIR; A01883; KIHUMK.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 111 119 FRAMEWORK-4.
FT DOMAIN 120 129 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC29 CRC64;
Query Match 80.7%; Score 457; DB 1; Length 129;
Best Local Similarity 86.9%; Pred. No. 7e-40;
Matches 93; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 1 DIQWTPSSLSASVGVGRVITTCRASQISNNLHMVYQKRGKAPKLIYASQISGVPS 60
1 DIQWTPSSLSASVGVGRVITTCRASQISNNLHMVYQKRGKAPKLIYASQISGVPS 60
Db 23 DIQWTPSSLSASVGVGRVITTCRASQISNNLHMVYQKRGKAPKLIYASQISGVPS 82
QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGGCTKVEIKR 107

Db 83 RFGSGSGTDFLTLLTSSLOPEDSATYCCQGSYTLTFPGGTVEIK 129

RESULT 7

KV1B HUMAN STANDARD; PRT; 108 AA.

AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 protein Au).";
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RX X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RT "The structure determination of the variable portion of the
 Bence-Jones protein Au.";
 RT Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.
 DR PIR; A91653; KIHUAD.
 DR PDB; 1JY5; 30-JUN-02.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KM
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6FB9 CRC64;

Query Match 79.5%; Score 450; DB 1; Length 108;
 Best Local Similarity 82.4%; Pred. No. 3e-39;
 Matches 89; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTITCRASOSISNNLHWYQOKGKAPKLLIYHASQSIGVPS 60
 Db 1 DIOMTSPSSLSASVGDRTITCRASODISDYNMTYQOKGKAPKLLIYDASNLSEGVPS 60

QY 61 RFGSGSGTDFLTLLTSSLOPEDPATYCCQGSNWPYTFPGGTVEIKR 108
 Db 61 RFGSGSGAHFTTISLSLOPEDLATYCCQGYDVLPTTFPGGTVEIKR 108

RESULT 8

KV1E HUMAN STANDARD; PRT; 108 AA.

AC P01597;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region DEE.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72053133; PubMed=5124396;
 RA Milstein C.P., Deverson E.V.;
 RT "The amino acid sequence of a human kappa light chain.";
 RT Biochem. J. 123:945-958(1971).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01865; KIHUDE.
 DR HSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.

KM
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 79.2%; Score 448; DB 1; Length 108;
 Best Local Similarity 79.6%; Pred. No. 4.8e-39;
 Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTITCRASOSISNNLHWYQOKGKAPKLLIYHASQSIGVPS 60
 Db 1 BIZMTSPSSLSASVGDRTITCRAGQSVKYLMTYQOKGKAPKLLIYFASLSKGVPS 60

QY 61 RFGSGSGTDFLTLLTSSLOPEDPATYCCQGSNWPYTFPGGTVEIKR 108
 Db 61 RFGSGSGTDFLTLLTSSLOPEDPATYCCQSYTTPTTFPGGTVEIKR 108

RESULT 9

KV1O HUMAN STANDARD; PRT; 108 AA.

AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
 and characterization of the tryptic peptides; the complete amino acid
 sequence of the protein; a contribution to the elucidation of the

RT three-dimensional structure of antibodies, in particular their
RT combining site." ;
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; Pubmed=1182131;
RA Bep O., Latman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Refi refined at 2.0-A resolution." ;
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1RE1; 17-FEB-84.
DR PDB; 1AR2; 12-NOV-87.
DR PDB; 1BW1; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT TURN 10 13
FT STRAND 15 16
FT TURN 19 25
FT STRAND 30 31
FT TURN 33 38
FT STRAND 40 41
FT TURN 44 49
FT STRAND 50 52
FT TURN 53 54
FT STRAND 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;
Query Match 78.8%; Score 446; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 7.6e-39;
Matches 87; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
Db 1 DIQWTSPPSSLSASVGRVITTCRASOSISNNLHWYQOKPKAPKLIYASOSISGVPS 60
1 DIQWTSPPSSLSASVGRVITTCRASODIKYLNWYQOTPEKAKLIYASNLQAGVPS 60
QY RFGSGSGTDTFTLTISLQPEDPATYTCQOSNSWPTFGGQTKVEIKR 108
61 RFGSGSGTDTYFTLTISLQPEDATYTCQOYQSLPYTFGGQTKQLITR 108
Db 61 RFGSGSGTDTYFTLTISLQPEDATYTCQOYQSLPYTFGGQTKQLITR 108
RESULT 10
KV1N HUMAN STANDARD; PRT; 108 AA.
ID KV1N HUMAN
AC P01606;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; Pubmed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains." ;
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01872; KIHUOU.
DR HSSP; P01607; 1RE1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;
Query Match 78.4%; Score 444; DB 1; Length 108;
Best Local Similarity 74.1%; Pred. No. 1.2e-38;
Matches 80; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
Db 1 DIQWTSPPSSLSASVGRVITTCRASOSISNNLHWYQOKPKAPKLIYASOSISGVPS 60
1 DIQWTSPPSSLSASVGRVITTCRASZTISYLBWYZKKPKAPBLIYASBLHSGVPS 60
QY RFGSGSGTDTFTLTISLQPEDPATYTCQOSNSWPTFGGQTKVEIKR 108
61 RFGSGSGTDTFTLTISLQPEDPATYTCQOSNSWPTFGGQTKVEIKR 108
Db 61 RFGSGSGTDTFTLTISLQPEDPATYTCQOSNSWPTFGGQTKVEIKR 108
RESULT 11
KV1P HUMAN STANDARD; PRT; 108 AA.
ID KV1P HUMAN
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; Pubmed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.)." ;
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]

RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hees M., Langer B., Ponstingl H.,
RA Steimetz-Kayne M., Suter L., Watanabe S.,
RL (1st) Frank F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR: A91638; KIHURY.
DR HSSP: P80362; IWTU.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDESA313DF3A CRC64;
Query Match 78.1%; Score 442; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 1.9e-38;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVITTCRASQISNNLHWYQOKRGPAPKLLIYASQISGVPS 60
DB 1 DIQMTQSPSSLSASVGRVITTCRASQISNNLHWYQOKRGPAPKLLIYASQISGVPS 60
QY 61 RFSGSGSGTFDTLTISLQPEDPATYCCQSNMWPYFGQGTVEIKR 108
DB 61 RFSGSGSGTFDTLTISLQPEDPATYCCQSNMWPYFGQGTVEIKR 108
RESULT 12
KVLS_HUMAN STANDARD; PRT; 108 AA.
ID KVL5_HUMAN
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Web.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
NP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Web).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR: A01877; KIHUMS.
DR HSSP: P80362; IWTU.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;
Query Match 78.1%; Score 442; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 1.9e-38;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVITTCRASQISNNLHWYQOKRGPAPKLLIYASQISGVPS 60
DB 1 DIQMTQSPSSLSASVGRVITTCRASQISNNLHWYQOKRGPAPKLLIYASQISGVPS 60
QY 61 RFSGSGSGTFDTLTISLQPEDPATYCCQSNMWPYFGQGTVEIKR 108
DB 61 RFSGSGSGTFDTLTISLQPEDPATYCCQSNMWPYFGQGTVEIKR 108
RESULT 13
KVLF_HUMAN STANDARD; PRT; 108 AA.
ID KVL5_HUMAN
AC P01558;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
NP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161 (1970).
RN [2]
RX DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gali W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196 (1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A90562; KIHURU.
DR HSSP: P01607; IRET.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2P4D88823 CRC64;

Query Match 77.9%; Score 441; DB 1; Length 108;
 Best Local Similarity 82.2%; Pred. No. 2.5e-38;
 Matches 88; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQWTPSSLSASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60
 1 DIQWTPSSLSASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60

DB 1 RFGSGSGTDTFTLTISSLOPEDPATYVCOQNSMWPYFGQTKVEIK 107
 61 RFGSGSGTDTFTLTISSLOPEDPATYVCOQNSMWPYFGQTKVEIK 107

RESULT 14

ID_KVID_HUMAN STANDARD; PRT; 108 AA.
 AC P01604;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Kue.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE
 RX MEDLINE=79237924; PubMed=112021;
 RA Eulitz M., Kley H.-P., Zeilner H.-J.;
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid
 sequence of the variable part of a human L-chain of the kappa-type.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A01870; KIHUKU.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12127 MW; 90679A5D90E4E98 CRC64;

Query Match 77.7%; Score 440; DB 1; Length 108;
 Best Local Similarity 79.6%; Pred. No. 3.1e-38;
 Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTPSSLSASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60
 1 DIQWTPSSLSASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60
 DB 1 RFGSGSGTDTFTLTISSLOPEDPATYVCOQNSMWPYFGQTKVEIK 108
 61 RFGSGSGTDTFTLTISSLOPEDPATYVCOQNSMWPYFGQTKVEIK 108
 DB 61 RFGSGSGTDTFTLTISSLOPEDPATYVCOQNSMWPYFGQTKVEIK 108

RESULT 15
 ID_KVID_HUMAN STANDARD; PRT; 107 AA.
 AC P01596;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region CAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE
 RX MEDLINE=75075135; PubMed=4216454;
 RA Mistein C.P., Deverson E.V.;
 RT "Primary structure of kappa light chain from a human myeloma
 protein";
 RL Eur. J. Biochem. 49:377-391(1974).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR; A01864; KIHUAR.
 DR HSSP; P80362; IWT.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; E1BFD0P9844C346 CRC64;

Query Match 77.7%; Score 439.5; DB 1; Length 107;
 Best Local Similarity 79.6%; Pred. No. 3.5e-38;
 Matches 86; Conservative 12; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIQWTPSSLSASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60
 1 DIQWTPSSLSASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60
 DB 1 RFGSGSGTDTFTLTISSLOPEDPATYVCOQNSMWPYFGQTKVEIK 108
 61 RFGSGSGTDTFTLTISSLOPEDPATYVCOQNSMWPYFGQTKVEIK 108
 DB 61 RFGSGSGTDTFTLTISSLOPEDPATYVCOQNSMWPYFGQTKVEIK 107

Search completed: May 13, 2004, 16:57:24
 Job time : 21.2143 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:43:32 ; Search time 22.7857 Seconds

(without alignments)
265.084 Million cell updates/sec

Title: US-09-910-483-5

Perfect score: 1 EVGLVSGGGLVQPGGSLRL.....TAGGYFAVYWGQGLTVTVSS 116

Sequence: 1 EVGLVSGGGLVQPGGSLRL.....TAGGYFAVYWGQGLTVTVSS 116

Scoring table: BIOSUM62

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	421.5	68.3	115	1	HV3D_HUMAN
2	421.5	68.2	122	1	HV3G_HUMAN
3	420.5	68.2	119	1	HV3I_HUMAN
4	412.5	66.9	115	1	HV3J_MOUSE
5	411	66.6	114	1	HV3B_HUMAN
6	406	65.8	116	1	HV3T_HUMAN
7	405.5	65.7	113	1	HV3H_HUMAN
8	405.5	65.7	113	1	HV27_MOUSE
9	404.5	65.6	113	1	HV31_MOUSE
10	402.5	65.2	142	1	HV01_RAT
11	401.5	65.1	115	1	HV03_MOUSE
12	401.5	65.0	136	1	HV16_MOUSE
13	399.5	64.7	113	1	HV28_MOUSE
14	398	64.5	120	1	HV3U_HUMAN
15	398	64.5	122	1	HV3A_HUMAN
16	397.5	64.4	121	1	HV3J_HUMAN
17	395.5	64.1	113	1	HV29_MOUSE
18	395.5	64.1	120	1	HV3E_HUMAN
19	394.5	63.9	115	1	HV3F_HUMAN
20	394.5	63.9	119	1	HV3L_HUMAN
21	393	63.7	119	1	HV3M_HUMAN
22	389	63.0	119	1	HV37_MOUSE
23	389	63.0	119	1	HV3N_HUMAN
24	389	63.0	122	1	HV21_MOUSE
25	386.5	62.6	123	1	HV18_MOUSE
26	385.5	62.5	116	1	HV05_CARAU
27	385	62.4	114	1	HV01_CANPA
28	384.5	62.3	117	1	HV17_MOUSE
29	384	62.2	117	1	HV3C_HUMAN
30	383	62.1	119	1	HV38_MOUSE
31	383	62.1	119	1	HV3P_HUMAN
32	382.5	62.0	123	1	HV19_MOUSE
33					

34	382	61.9	119	1	HV40_MOUSE	P01810 mus musculus
35	381.5	61.8	123	1	HV25_MOUSE	P01794 mus musculus
36	381	61.8	126	1	HV2K_HUMAN	P01772 homo sapien
37	379.5	61.5	123	1	HV22_MOUSE	P01781 mus musculus
38	379.5	61.5	123	1	HV24_MOUSE	P01793 mus musculus
39	377.5	61.2	123	1	HV23_MOUSE	P01792 mus musculus
40	377	61.1	117	1	HV3O_HUMAN	P01776 homo sapien
41	375.5	60.9	117	1	HV42_MOUSE	P01812 mus musculus
42	375	60.8	111	1	HV35_MOUSE	P01804 mus musculus
43	373.5	60.5	118	1	HV39_MOUSE	P01809 mus musculus
44	373	60.5	122	1	HV20_MOUSE	P01789 mus musculus
45	369.5	59.9	144	1	HV26_MOUSE	P01795 mus musculus

ALIGNMENTS

RESULT 1	ID	HV3D_HUMAN	STANDARD:	PRT:	115 AA.
AC	P01765	1986 (Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Ig heavy chain V-II region TIL.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=78005528; PubMed=409716;				
RA	Wang A.-C., Wang I.Y., Rudenberg H.H.;				
RT	"Immunoglobulin structure and genetics. Identity between variable				
RL	J. Biol. Chem. 252:7192-7199 (1977).				
CC	-I- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS				
CC	OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL				
CC	GAMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO				
CC	IDENTICAL.				
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A02048; H3HUTL.				
DR	HSSP; P01772; 2P84.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; Igv; 1.				
DR	PROSITE; PS50835; IG LIKE; 1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 108				
FT	NON TER 115				
SQ	SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;				
Query Match	68.3%;	Score 421.5;	DB 1;	Length 115;	
Best Local Similarity	70.6%;	Pred. No. 1.3e-36;			
Matches	84;	Conservative	9;	Mismatches 19;	Indels 7;
Gaps	2;				
QY	1	EVGLVSGGGLVQPGGSLRLSCAASGFINIDTYIHVYRQAPGKGLFWARIDPANDTIY 60			
DB	1	EVGLVSGGGLVQPGGSLRLSCAASGFTFTYMSVYRQAPGKGLZNVGALZGLSVSZSY 60			
QY	61	ADSVKGRFTISDDSKNTAVLYQNSLRAEDTAVYYCT--ASGYFAVYWGQGLTVTVSS 116			
DB	61	ABSVKGRFTISDDSKNTAVLYQNSLRAEDTAVYYCT--ASGYFAVYWGQGLTVTVSS 115			
RESULT 2					
HV3G_HUMAN	STANDARD;	PRT;	122 AA.		
ID	P01768;				

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region CAM.
 OS Homo sapiens (human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81013859; PubMed=6774332;
 RA Lehman D.W., Putnam F.W.;
 RT "Amino acid sequence of the variable region of a human mu chain:
 RT location of a possible CH segment."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
 CC PATIENT WITH MACROGLOBULINEMIA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02051; MAHUM.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1
 FT NON_TER 122
 FT SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
 SQ
 Query Match 68.2%; Score 421; DB 1; Length 122;
 Best Local Similarity 67.2%; Pred. No. 1.5e-36;
 Matches 82; Conservative 13; Mismatches 21; Indels 6; Gaps 2;
 QY 1 EVQLVESGGGVQPGGSLRLSCAASGFRNIKDTYIMHWQAQPKGLEWVARIDPANDNTITY 60
 DB 1 QVQLVESGGGVQPGGSLRLSCAASGFRNIKDTYIMHWQAQPKGLEWVARISYGBBKRY 60
 QY 61 ADSVKGRTFTSSDSDSKNTAYLQNSLRADTAIVYCTA---GYW--FAVWGCTLTAVT 114
 DB 61 ADSVKGRTFTSSDSDSKNTAYLQNSLRADTAIVYCTA---GYW--FAVWGCTLTAVT 120
 QY 115 SS 116
 DB 121 SS 122
 DB
 RESULT 3
 HV31 HUMAN STANDARD; PRT; 119 AA.
 ID HV31 HUMAN STANDARD; PRT; 119 AA.
 AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region NIF.
 OS Homo sapiens (human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The
 RT chymotryptic peptides of the H-chain, alignment of the tryptic
 RT peptides and discussion of the complete structure."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 RN [2]

RP DISULFIDE BOND.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA
 CC PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A91668; GHUM1.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1
 FT NON_TER 22
 FT DISULFID 22 96
 FT SEQUENCE 119 AA; 13242 MW; C96935A6B55E165B CRC64;
 SQ
 Query Match 68.2%; Score 420.5; DB 1; Length 119;
 Best Local Similarity 69.7%; Pred. No. 1.7e-36;
 Matches 83; Conservative 10; Mismatches 23; Indels 3; Gaps 1;
 QY 1 EVQLVESGGGVQPGGSLRLSCAASGFRNIKDTYIMHWQAQPKGLEWVARIDPANDNTITY 60
 DB 1 QVQLVESGGGVQPGGSLRLSCAASGFRNIKDTYIMHWQAQPKGLEWVARISYGBBKRY 60
 QY 61 ADSVKGRTFTSSDSDSKNTAYLQNSLRADTAIVYCTA---SGYFAVWGCTLTAVTSS 116
 DB 61 ADSVKGRTFTSSDSDSKNTAYLQNSLRADTAIVYCTA---SGYFAVWGCTLTAVTSS 119
 QY 115 SS 116
 DB 121 SS 122
 DB
 RESULT 4
 HV32 MOUSE STANDARD; PRT; 115 AA.
 ID HV32 MOUSE STANDARD; PRT; 115 AA.
 AC P01801;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region J606.
 OS Mus musculus (mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82099361; PubMed=6798111;
 RA Johnson N., Stankard J., Paul L., Hood L.;
 RT "The complete V domain amino acid sequences of two myeloma inulin-
 RT binding proteins."
 RL J. Immunol. 128:302-307(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS INULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; C92811; AWM506.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 114
 FT DISULFID 22 98
 FT BY SIMILARITY.

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FT  NON TER      115      115
SQ  SEQUENCE      115 AA; 12810 MM; B67AD6638A121ASF CRC64;

Query Match
Best Local Similarity 66.9%; Score 412.5; DB 1; Length 115;
Matches 80; Conservative 16; Mismatches 17; Indels 5; Gaps 2;

QY  1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRAQPGKLEWVARIDPANDN--T 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  1 EVKLSEGGGLVPGGSLRLSCAASGFTFSPNYMMWRQSEKLEWVAELRLSNRYAT 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY  59 IYADSVKGRFTISSDSKNTAYLQNMNSLRADPTAVYCTASGYFAYWGQGLTVTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  61 HYAESVKGRTFTISRDSSKSSVYLQMNNLRADDTGIYCTTG---FAYWGQGLTVTVSA 115
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
HV3H HUMAN      STANDARD;      PRT;      114 AA.
ID  P01763;
AC  P01763;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig heavy chain V-II region WEA.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  MEDLINE=83273707; PubMed=6410398;
RX  Goni F., Frangione B.;
RT  "Amino acid sequence of the Fv region of a human monoclonal Igm
RT  (protein WEA) with antibody activity against 3,4-pyruvylated
RT  galactose in Klebsiella polysaccharides K30 and K33.";
RL  Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC  -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC  AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC  WALDENSTROM'S MACROGLOBULINEMIA.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  HSP; P01772; 2PB4.
DR  HSP; A02046; M3HUGA.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; P:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig_V.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Ig; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region; Fyrtolidone carboxylic acid.
FT  DOMAIN 1 112 IG-LIKE.
FT  MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT  NON TER 114 114
SQ  SEQUENCE 114 AA; 12256 MM; D88234PB418A07B7 CRC64;

Query Match
Best Local Similarity 66.6%; Score 411; DB 1; Length 114;
Matches 81; Conservative 13; Mismatches 20; Indels 2; Gaps 2;

QY  1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  1 QVQLVDSGGGLVPGGSLRLSCASGFTFSPNDMMWRQAPGKLEWVSLFGSGSGLTIYV 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY  61 ADSVKGRFTISDSDSKNTAYLQNMNSLRADPTAVYCTASGYFAYWGQGLTVTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  61 ADSVKGRFTISRNBSKNSLYLQNMNSLRADPTAVYCTA--ARQ--WLMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
HV3H HUMAN      STANDARD;      PRT;      116 AA.
ID  P01761;
AC  P01761;

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DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig heavy chain V-II region GHL.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  MEDLINE=75059123; PubMed=4803843;
RX  Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;
RT  "The primary structure of a monoclonal Igm-immunoglobulin
RT  (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT  type), subgroup H III. Architecture of the complete Igm-molecule.";
RL  Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN  [2]
RP  REVISION TO 28-33.
RA  Hilschmann N.;
RL  Submitted (JUN-1975) to the PIR data bank.
CC  -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC  MACROGLOBULIN.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  HSP; P01772; 2PB4.
DR  HSP; A02064; M3HUGL.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; P:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig_V.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Ig; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 112 IG-LIKE.
FT  NON TER 116 116
SQ  SEQUENCE 116 AA; 12730 MM; 2C67CA9A9AAA1282 CRC64;

Query Match
Best Local Similarity 65.8%; Score 406; DB 1; Length 116;
Matches 80; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

QY  1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  1 EVOLVESGGGLVPGGSLRLSCAASGFTFSPNLTWRAQPGKLEWVAIKZBGSZBZY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY  61 ADSVKGRFTISDSDSKNTAYLQNMNSLRADPTAVYCTASGYFAYWGQGLTVTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  61 VDSVKGRFTISRDNAKNSLYLQNMNSLRADPTALYTCARWGCGDYGQGLTVTVST 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
HV3H HUMAN      STANDARD;      PRT;      122 AA.
ID  P01769;
AC  P01769;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig heavy chain V-III region GA.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  MEDLINE=74175307; PubMed=4208843;
RX  Florent G., Lehman D., Putnam F.W.;
RT  "The switch point in mu heavy chains of human Igm immunoglobulins.";
RL  Biochemistry 13:2482-2498(1974).
CC  -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC  MACROGLOBULIN.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  PIR; A02052; M3HUGA.

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DR HSSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; F:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR Immunoglobulin V region; Fyrtolidone carboxylic acid.
 KW DOMAIN 1 112
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON TER 122 122
 SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 65.8%; Score 406; DB 1; Length 122;
 Best Local Similarity 61.5%; Pred. No. 5.3e-35;
 Matches 75; Conservative 18; Mismatches 23; Indels 6; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGMLSCAASGFNIKDTYIHWVROAPGKLEWVA--RIDPANDNT 60
 DB 1 QVZLVZSGGAVZPRSRSLRLSCAASGFSTYNAHWVROAKGKLZMLSVSYGEBZLY 60
 QY 61 ADSVKGRTTSSDSSKNTAVYLOMNSLRAPDAVYCTASGYWFA-----YMGQGLTVT 114
 DB 61 AASVKGRTTISRBSKNTAVYLOMNSLRAPDAVYCTASGYWFA-----YMGQGLTVT 120
 QY 115 SS 116
 DB 121 SS 122

RESULT 8
 HV27_MOUSE STANDARD; PRT; 113 AA.
 AC P01756; 2PB4.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region A4.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78158406; PubMed=417344;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Sequence variation among heavy chains from inulin-binding myeloma
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS INULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A93818; AVMSAB.
 DR HSSP; P01810; 2PB4.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 >113
 FT DISULFID 22 98
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 65.7%; Score 405.5; DB 1; Length 113;
 Best Local Similarity 68.1%; Pred. No. 5.5e-35;
 Matches 79; Conservative 14; Mismatches 18; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVOPGSGMLSCAASGFNIKDTYIHWVROAPGKLEWVA--RIDPANDNT 58
 DB 1 EVOLVESGGGLVOPGSGMLSCAASGFNIKDTYIHWVROAPGKLEWVA--RIDPANDNT 58

DB 1 EVKLEBSGGGLVOPGSGMLSCAASGFSTSNYMMNWRQSPKGLWEVAEIRLKSHTYAT 60
 QY 59 IYADSVKGRFTTSSDSSKNTAVYLOMNSLRAPDAVYCTASGYWFAVWGQGLTVT 114
 DB 61 HYAESVKGRTTISRBSKNTAVYLOMNSLRAPDAVYCTASGYWFAVWGQGLTVT 113

RESULT 9
 HV30_MOUSE STANDARD; PRT; 113 AA.
 ID HV30_MOUSE
 AC P01799;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region ABE-47N.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77134726; PubMed=402936;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
 RT protein.";
 RL Biochemistry 16:1170-1175 (1977).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS INULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A90400; AVMSB7.
 DR HSSP; P01810; 2PB4.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 >113
 FT DISULFID 22 98
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 65.7%; Score 405.5; DB 1; Length 113;
 Best Local Similarity 68.1%; Pred. No. 5.5e-35;
 Matches 79; Conservative 15; Mismatches 17; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVOPGSGMLSCAASGFNIKDTYIHWVROAPGKLEWVA--RIDPANDNT 58
 DB 1 EVKLEBSGGGLVOPGSGMLSCAASGFSTSNYMMNWRQSPKGLWEVAEIRLKSHTYAT 60
 QY 59 IYADSVKGRFTTSSDSSKNTAVYLOMNSLRAPDAVYCTASGYWFAVWGQGLTVT 114
 DB 61 HYAESVKGRTTISRBSKNTAVYLOMNSLRAPDAVYCTASGYWFAVWGQGLTVT 113

RESULT 10
 HV31_MOUSE STANDARD; PRT; 113 AA.
 ID HV31_MOUSE
 AC P01800;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region T957.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81216632; PubMed=6787122;
 RA Rudikoff S., Potter M.;
 RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
 RT evidence for a new heavy chain joining segment.";

RL J. Immunol. 127:191-194(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS INULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A92810; AVMS57.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 >113 IG-LIKE.
 FT DISULFID 22 BY SIMILARITY.
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12732 MW; 26618P626B59859E CRC64;
 Query Match 65.6%; Score 404.5; DB 1; Length 113;
 Best Local Similarity 68.1%; Pred. No. 7e-35;
 Matches 79; Conservative 13; Mismatches 19; Indels 5; Gaps 2;
 QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVA--RIDPANDNT 58
 DB 1 EVKLEESGGGLVOPGSGMKLSCVAGFTFSYNNWNRQSPDEKGLEWVAEIRLKSHTYET 60
 QY 59 IYADSVKGRFTISDDSKNTAYLQMNSLRAEDTAVVYCTASGYFAYMGQGLTVTV 114
 DB 61 HYASVKGRTTISRDKSSVYLQMNILRAEDTGYCTTG--FAVMGQGLTVTV 113
 RESULT 11
 HVO1 RAT STANDARD; PRT; 142 AA.
 AC P01805;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region IR2 precursor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Petersson U., Engstrom A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E";
 RL Nucleic Acids Res. 10:6041-6049(1982).
 CC -1- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
 CC IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/MSL RATS.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02075; EVRTR2.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.
 FT DOMAIN 20 133 IG-LIKE.
 FT NON TER 142 142
 SQ SEQUENCE 142 AA; 16024 MW; DE29B6CEB745DF3B CRC64;
 Query Match 65.2%; Score 402.5; DB 1; Length 142;
 Best Local Similarity 63.4%; Pred. No. 1.5e-34;
 Matches 78; Conservative 15; Mismatches 23; Indels 7; Gaps 3;
 QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVAIRIDPANDNTI- 59
 DB 20 EVKLEESGGGLVOPGSGMKLSCVAGFTFSYNNWNRQAPGKGLEWVAEIRLNANNYYVA 79

QY 60 -YADSVKGRFTISDDSKNTAYLQMNSLRAEDTAVVYCTASGYFAYMGQGLTVTV 113
 DB 80 YKSKLGRFTTISRDKSSVYLQMNIRSEDTGYCTTG--FAVMGQGLTVTV 139
 QY 114 VSS 116
 DB 140 VSS 142
 RESULT 12
 HVI3 MOUSE STANDARD; PRT; 115 AA.
 ID HVI3 MOUSE
 AC P01802;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region W3082.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82099361; PubMed=6798111;
 RA Johnson N., Slankard J., Paul L., Hood L.;
 RT "The complete V domain amino acid sequences of two myeloma inulin-
 binding proteins";
 RL J. Immunol. 128:302-307(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS INULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; D92811; AVMS82.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 114 IG-LIKE.
 FT DISULFID 22 98 BY SIMILARITY.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121CSA CRC64;
 Query Match 65.1%; Score 401.5; DB 1; Length 115;
 Best Local Similarity 66.1%; Pred. No. 1.5e-34;
 Matches 78; Conservative 16; Mismatches 19; Indels 5; Gaps 2;
 QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWRQAPGKGLEWVA--RIDPANDNT 58
 DB 1 EVKLEESGGGLVOPGSGMKLSCVAGFTFSYNNWNRQSPDEKGLEWVAEIRLKSHTYAT 60
 QY 59 IYADSVKGRFTISDDSKNTAYLQMNSLRAEDTAVVYCTASGYFAYMGQGLTVTVSS 116
 DB 61 HYASVKGRTTISRDKSSVYLQMNIRSEDTGYCTTG--FAVMGQGLTVTVSSA 115
 RESULT 13
 HVI6 MOUSE STANDARD; PRT; 136 AA.
 ID HVI6 MOUSE
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;

RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 RN [2]
 RP SEQUENCE OF 17-136.
 RX MEDLINE=7100368; PubMed=401950;
 RA Aetungbo K., Mistein C., Secher D.S.;
 RT "Molecular analysis of spontaneous somatic mutants."
 RL Nature 265:299-304(1977).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; J00522; A015290.1; -;
 DR PIR; E08089; GIMS21.
 DR PDB; 1IGC; 03-JUN-95.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KM Immunoglobulin V region; Signal; 3D-structure.
 FT NON_TER 1
 FT SIGNAL 1
 FT CHAIN 16
 FT DOMAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
 FT DOMAIN 115 119 D SEGMENT.
 FT DOMAIN 120 136 JH4 SEGMENT.
 FT DISULFID 38 112
 FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
 FT CONFLICT 89 90 DN -> ND (IN REF. 2).
 FT CONFLICT 115 115 W -> H (IN REF. 2).
 FT CONFLICT 120 120 Y -> W (IN REF. 2).
 FT NON_TER 136
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;
 Query Match 65.0%; Score 401; DB 1; Length 136;
 Best Local Similarity 66.7%; Pred. No. 2e-34;
 Matches 80; Conservative 9; Mismatches 27; Indels 4; Gaps 1;
 QY 1 EVOLVESGGGLVOPGSGRLRLSCAASGFENIKDITYHWRAQAPGKLEWVARIDPANDNTY 60
 DB 17 DVLVESGGGLVOPGSGRLRLSCAASGFENIKDITYHWRAQAPGKLEWVARIDPANDNTY 76
 QY 61 ADVSKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASG---YWPAYWGQGLLVTV 116
 DB 77 ADVKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASG---YWPAYWGQGLLVTV 136
 RESULT 14
 HV28 MOUSE STANDARD; PRT; 113 AA.
 ID HV28 MOUSE
 AC P01797;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region U61.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76158406; PubMed=417344;
 RA Virena M., Rudnikoff S., Potter M.;
 RT "Sequence variation among heavy chains from inulin-binding myeloma
 RT proteins.";

RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS INULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; B93818; AWM561.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 >113 IG-LIKE.
 FT DISULFID 22 98 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;
 Query Match 64.7%; Score 399.5; DB 1; Length 113;
 Best Local Similarity 67.2%; Pred. No. 2.3e-34;
 Matches 78; Conservative 14; Mismatches 19; Indels 5; Gaps 2;
 QY 1 EVOLVESGGGLVOPGSGRLRLSCAASGFENIKDITYHWRAQAPGKLEWVA--RIDPANDNT 58
 DB 1 EVLLESGGGLVOPGSGRLRLSCAASGFENIKDITYHWRAQAPGKLEWVAIRIKSHNYAT 60
 QY 59 IYADSVKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGWPAYWGQGLLVTV 114
 DB 61 HYAESVKGRTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGWPAYWGQGLLVTV 113
 RESULT 15
 HV3U HUMAN STANDARD; PRT; 120 AA.
 ID HV3U HUMAN
 AC P01782;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region DOB.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80020921; PubMed=114209;
 RA Steiner L.A., Garcia Pardo A., Margolies M.N.;
 RT "Amino acid sequence of the heavy-chain variable region of the
 RT crystallizable human myeloma protein DOB.";
 RL Biochemistry 18:4068-4080(1979).
 RN [2]
 RP CRYSTALLIZATION.
 RX MEDLINE=80020920; PubMed=114208;
 RA Steiner L.A., Lopes A.D.;
 RT "The crystallizable human myeloma protein DOB has a hinge-region
 RT deletion.";
 RL Biochemistry 18:4054-4067(1979).
 CC -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
 CC HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
 CC DISULFIDE BONDS.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A90431; GHUDB.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 112 IG-LIKE.
 FT NON_TER 120 120

SQ SEQUENCE 120 AA; 13440 MM; 880DDE307C4B2627 CRC64;

Query Match 64.5%; Score 398; DB 1; Length 120;

Best local Similarity 66.1%; Pred. No. 3.5e-34;

Matches 80; Conservative 10; Mismatches 25; Indels 6; Gaps 2;

QY 1 EVQLVESGGGLVOPGSGLRISCAASGFNIDKTYIHWRQAPGKGLEWVARIDPANDNTIY 60

Db 1 EVQLVESGGDLVOPGSRSLRISCAASGFNPFHEHNNMHLRQPGKGPENWSTITWNGSVLY 60

QY 61 ADSYKGRFTISSDPSDKNTATLQMSLRPQDTAVYYCTASG-----WPAIWGGTILVTVS 115

Db 61 ADSYKGRFAISRDNQAQKTLTLQILIRPEDTAFYYC-AKGYIWNQNWPFDSWGCGTILVTVS 119

QY 116 S 116

Db 120 S 120

Search completed: May 13, 2004, 16:57:24

Job time : 23.7857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:56:47 ; Search time 37.125 Seconds
(without alignments)
279,830 Million cell updates/sec

Title: A1 US-09-910-483-7

Perfect score: 566

Sequence: 1 DIQMTQSPSSLSASVDGRVT.....QQSNMPTFGQGTKEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 78:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	490	86.6	127	2	S40367	Ig kappa chain V-J
2	483	85.3	123	2	S40331	Ig kappa chain - h
3	482	85.2	108	2	B49047	Ig kappa chain V r
4	480	84.8	129	2	S40369	Ig kappa chain - h
5	479	84.6	125	2	S40333	Ig kappa chain V-J
6	474	83.7	108	2	S19674	Ig kappa chain V r
7	471	83.2	108	2	S44122	Ig kappa chain V r
8	470	83.0	125	2	S40349	Ig kappa chain V-J
9	469	82.9	117	2	S46371	Ig kappa chain V-J
10	468	82.7	122	2	S40370	Ig kappa chain - h
11	465	82.2	108	1	K1HUBN	Ig kappa chain V-I
12	464	82.0	109	2	S31998	Ig kappa chain - h
13	463	81.8	107	2	S36269	Ig kappa chain V
14	463	81.8	108	1	K1HUBU	Ig kappa chain V-I
15	463	81.8	120	2	S46370	Ig kappa chain V-J
16	463	81.8	123	2	S40313	Ig kappa chain V-J
17	462	81.6	125	2	S40353	Ig kappa chain V-J
18	462	81.6	131	2	S40352	Ig kappa chain V-J
19	461	81.4	108	1	K1HUBU	Ig kappa chain V-I
20	461	81.4	117	2	S46376	Ig kappa chain V-J
21	461	81.4	125	2	S40316	Ig kappa chain - h
22	460	81.3	108	1	K1HUBU	Ig kappa chain V-I
23	460	81.3	108	2	S47182	Ig kappa chain V-I
24	459.5	81.2	124	2	S40336	Ig kappa chain V-J
25	459	81.1	107	2	S36262	Ig kappa chain V
26	459	81.1	109	2	S31981	Ig kappa chain - h
27	459	81.1	132	2	S40334	Ig kappa chain - h
28	458.5	81.0	125	2	S40315	Ig kappa chain - h
29	458	80.9	107	2	S36264	Ig lambda chain V

30	458	80.9	108	1	K1HUBE	Ig kappa chain V-I
31	457	80.7	129	1	K1HUMK	Ig kappa chain pre
32	456	80.6	139	2	S40317	Ig kappa chain - h
33	455	80.4	126	2	S40335	Ig kappa chain V-J
34	454.5	80.3	107	2	S36275	Ig kappa chain V
35	452	79.9	122	2	S40314	Ig kappa chain - h
36	452	79.9	129	2	S52793	Ig kappa chain V r
37	450	79.5	107	2	JL0139	Ig kappa chain V r
38	450	79.5	108	1	K1HUBU	Ig kappa chain V-I
39	450	79.5	108	2	S36279	Ig kappa chain V
40	450	79.5	129	2	S52792	Ig kappa chain V r
41	449.5	79.4	106	2	PC2397	anti-tetanus toxin
42	449	79.3	130	2	S40368	Ig kappa chain - h
43	448	79.2	108	1	K1HUBE	Ig kappa chain V-I
44	447	79.0	125	2	S40350	Ig kappa chain - h
45	447	79.0	128	2	S46372	Ig kappa chain var

ALIGNMENTS

RESULT 1

S40367
Ig kappa chain V-J-C region - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40367

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40367

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-127 <KLE>

C/Cross-references: EMBL:X72477

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/33-107/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 86.6%; Score 490; DB 2; Length 127; Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy	1	DIQMTQSPSSLSASVDGRVTITTCRASQISNNLHWYQKRGKAPKLIYASQISGVPS	60
Db	18	DIQMTQSPSSLSASVDGRVTITTCRASQISNNLHWYQKRGKAPKLIYASQISGVPS	77
Qy	61	RFSGSGSGTDFTLTISLQPEDPATYCCQOSNMPYFGQGTKEIKR	108
Db	78	RFSGSGSGTDFTLTISLQPEDPATYCCQOSNMPYFGQGTKEIKR	125

RESULT 2

S40331
Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40331

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40331

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-123 <KLE>

C/Cross-references: EMBL:X72441; NID:G441350; PIDN:CA51109.1; PID:G441351

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 483; DB 2; Length 123;

submitted to the EMBL Data Library, March 1994

A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A:Reference number: S44105

A:Accession: S44122

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-108 <HAM>

A:Cross-references: EMBL:Z31390; NID:9472976; PIDN:CAA83265.1; PID:9440533

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 471; DB 2; Length 108;

Best Local Similarity 88.0%; Pred. No. 3,1e-32;

Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQKPKKLIYHASQISGVPS 60

DB 1 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQKPKKLIYHASQISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

DB 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

RESULT 8

S40349

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S40349

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Status: Preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72459; NID:9441386; PIDN:CAA51127.1; PID:9441387

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 470; DB 2; Length 125;

Best Local Similarity 86.9%; Pred. No. 4.2e-32;

Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 IOMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQKPKKLIYHASQISGVPS 61

DB 19 IOMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQKPKKLIYHASQISGVPS 78

QY 62 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

DB 79 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 125

RESULT 9

S46371

Ig kappa chain V-J region (T24-3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C:Accession: S46371; S38645

R:Bensimon, C.; Chastagner, P.; Zouali, M.

EMBL J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reas

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46371

A:Molecule type: mRNA

A:Residues: 1-117 <BEN>

A:Cross-references: EMBL:Z27172; NID:9415959; PIDN:CAA81696.1; PID:9415960

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 469; DB 2; Length 117;

Best Local Similarity 85.5%; Pred. No. 4.8e-32;

Matches 94; Conservative 6; Mismatches 8; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQKPKKLIYHASQISGVPS 60

DB 8 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQKPKKLIYHASQISGVPS 67

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

DB 68 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 117

RESULT 10

S40370

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40370

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40370

A:Status: Preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-122 <KLE>

A:Cross-references: EMBL:X72480; NID:9441428; PIDN:CAA51148.1; PID:9441429

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 468; DB 2; Length 122;

Best Local Similarity 87.0%; Pred. No. 6.1e-32;

Matches 94; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQKPKKLIYHASQISGVPS 60

DB 15 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQKPKKLIYHASQISGVPS 74

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

DB 75 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 122

RESULT 11

K1HUBN

Ig kappa chain V-I region (Ban) - human

C:Species: Homo sapiens (man)

C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 15-Aug-1997

C:Accession: A01878

R:Dwulet, F.E.; O'Connor, T.P.; Benson, M.D.

Mol. Immunol. 23, 73-78, 1986

A:Title: Polymorphism in a kappa I primary (AI) amyloid protein (BAN).

A:Reference number: A01878; MUID:86174817; PMID:3083240

A:Accession: A01878

A:Molecule type: protein

A:Residues: 1-108 <DWU>

C:Genetics:

A:Gene: GDB:IGKVL

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: amyloid; heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:35-49/Region: complementarity-determining 1

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-107/Region: framework 4
F:23-68/Disulfide bonds: #status predicted

Query Match 82.2%; Score 465; DB 1; Length 108;
Best Local Similarity 83.3%; Pred. No. 9.5e-32;
Matches 90; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITTCRASQSISSNNLHWYQKRGKAPKLLIYHASQISGVPS 60
Db 1 DIQLTQSPSSLSASVGDRTITTCRASQSISSNNLHWYQKRGKAPKLLIYDSTLQSGVPS 60

QY 61 RFSGSGSGTDFLTITLSSLOPEDFATYYCOQSNMWPYTFGQGTVEIKR 108
Db 61 RFSGSGSGTDFLTITLSSLOPEDFATYYCOQSNMWPYTFGQGTVEIKR 108

RESULT 12

S31998
Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C/Accession: S31998

R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

Submitted to the EMBL Data Library, June 1992

A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A/Reference number: S31977

A/Accession: S31998

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <PDR>

C/Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 464; DB 2; Length 109;
Best Local Similarity 85.2%; Pred. No. 1.2e-31;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITTCRASQSISSNNLHWYQKRGKAPKLLIYHASQISGVPS 60
Db 1 ELVMTQSPSSLSASVGDRTITTCRASQSISSNNLHWYQKRGKAPKLLIYASSTLQSGVPS 60

QY 61 RFSGSGSGTDFLTITLSSLOPEDFATYYCOQSNMWPYTFGQGTVEIKR 108
Db 61 RFSGSGSGTDFLTITLSSLOPEDFATYYCOQSNMWPYTFGQGTVEIKR 108

RESULT 13

S36269
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C/Accession: S36269

R/Gilfiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36266; MUID:93178448; PMID:7679990

A/Accession: S36269

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-107 <GGI>

A/Cross-references: EMBL:Z18838; NID:G33422; PIDN:CAA79290.1; PID:G939915

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 463; DB 2; Length 107;
Best Local Similarity 85.0%; Pred. No. 1.4e-31;
Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITTCRASQSISSNNLHWYQKRGKAPKLLIYHASQISGVPS 60
Db 1 DIOMTQSPSSLSASVGDRTITTCRASQSISSNNLHWYQKRGKAPKLLIYGTSLQSGVPS 60

QY 61 RFSGSGSGTDFLTITLSSLOPEDFATYYCOQSNMWPYTFGQGTVEIKR 107
Db 61 RFSGSGSGTDFLTITLSSLOPEDFATYYCOQSNMWPYTFGQGTVEIKR 107

RESULT 14

K1H0HU
Ig kappa chain V-I region (Hau) - human

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1994 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000

C/Accession: A01868; S02574

R/Matnabe, S.; Hillebrand, N.

Hope-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970

A/Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg

A/Reference number: A01868; MUID:71032830; PMID:4097974

A/Accession: A01868

A/Molecule type: protein

A/Residues: 1-108 <MAT>

A/Note: the C region of this chain has the Inv (3) marker

R/Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987

A/Title: Chemical modification of the carboxyl groups of protein substrates enhances thei

A/Reference number: S02572; MUID:88005152; PMID:3115831

A/Contents: annotation

C/Comment: This is a Bence Jones protein.

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

C/Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kappa)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

F:23-88/Disulfide bonds: #status predicted

Query Match 81.8%; Score 463; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 1.4e-31;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITTCRASQSISSNNLHWYQKRGKAPKLLIYHASQISGVPS 60
Db 1 DIOMTQSPSSLSASVGDRTITTCRASQSISSNNLHWYQKRGKAPKLLIYASSTLQSGVPS 60

QY 61 RFSGSGSGTDFLTITLSSLOPEDFATYYCOQSNMWPYTFGQGTVEIKR 108
Db 61 RFSGSGSGTDFLTITLSSLOPEDFATYYCOQSNMWPYTFGQGTVEIKR 108

RESULT 15

S46370
Ig kappa chain V-J region (T23-9) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C/Accession: S46370; S38644

R/Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reat

A/Reference number: S46369; MUID:94313975; PMID:8039491

A/Accession: S46370

A/Molecule type: mRNA

A/Residues: 1-120 <BN>

A/Cross-references: EMBL:Z27171; NID:G415957; PIDN:CAA61695.1; PID:G415958

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 463; DB 2; Length 120;
Best Local Similarity 85.5%; Pred. No. 1.5e-31;

Matches 94; Conservative 6; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDGVITTCRASQISNNLHWQOKPKKLIYHASQISGVPS 60
 |||||
 Db 11 DIQMTQSPSSLSASVGDGVITTCRASRSISFLNMYQOKPKAPOLLIVAVSRLOSGVPS 70
 |||||

Qy 61 RFGSGSGGTDFTLLISSLQPEDFATYYCOQSNWSP--YTFGGGTKEIKR 108
 |||||
 Db 71 RFGSGSGGTDFTLLISSLQPEDFATYYCOQSFNPPETFGGTKEIKR 120
 |||||

Search completed: May 13, 2004, 17:03:14
 Job time : 38.125 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:56:47 ; Search time 39.875 Seconds

(without alignments)
279.830 Million cell updates/sec

Title: US-09-910-483-5

Perfect score: 617
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....TASGYWFAWGQGTLLTVSS 116

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458.5	74.3	119	2	S31107 Ig heavy chain - h
2	452.5	73.3	117	2	S31109 Ig heavy chain - h
3	452.5	73.3	119	2	C36005 Ig heavy chain V r
4	451.5	73.2	140	2	S31588 Ig heavy chain V r
5	450.5	73.0	121	2	S19666 Ig heavy chain V r
6	448	72.6	120	2	S48798 Ig heavy chain V r
7	447.5	72.5	138	2	S31666 Ig heavy chain V r
8	446.5	72.4	119	2	D36005 Ig heavy chain V r
9	446.5	72.4	143	2	S23624 Ig heavy chain V r
10	445.5	72.3	140	2	S70442 Ig heavy chain pre
11	445.5	72.2	123	2	S31114 Ig heavy chain - h
12	445	72.1	114	2	S31120 Ig heavy chain - h
13	445	72.1	114	2	S46350 Ig heavy chain V r
14	444.5	72.0	125	2	S30531 Ig heavy chain V r
15	444	72.0	120	2	S44111 Ig heavy chain V-D
16	444	72.0	128	2	S26786 Ig heavy chain V r
17	443.5	71.9	135	2	S31598 Ig heavy chain V r
18	442	71.6	124	2	S20782 Ig heavy chain V r
19	441.5	71.6	132	2	S31603 Ig heavy chain V r
20	438.5	71.1	119	2	S31108 Ig heavy chain - h
21	438	71.0	139	2	PC1213 Ig heavy chain pre
22	437.5	70.9	140	2	S31686 Ig heavy chain V r
23	436.5	70.7	127	2	S38489 Ig heavy chain - h
24	436	70.7	139	2	S31674 Ig heavy chain V r
25	436	70.7	147	2	I17780 Ig variable region
26	435.5	70.6	120	2	S36273 Ig heavy chain V r
27	435.5	70.6	121	2	G36005 Ig heavy chain V r
28	435	70.5	128	2	S26790 Ig heavy chain V r
29	434.5	70.4	121	2	S26798 Ig heavy chain V r

30	434.5	70.4	121	2	I55673 Ig heavy chain - h
31	434	70.3	122	2	S31117 Ig heavy chain - h
32	433.5	70.3	120	2	S36278 Ig heavy chain V r
33	433.5	70.3	130	2	S31601 Ig heavy chain V r
34	433	70.2	116	2	S31110 Ig heavy chain - h
35	433	70.2	128	2	S48797 Ig heavy chain V r
36	432	70.0	118	2	S31116 Ig heavy chain - h
37	431.5	69.9	121	2	S31104 Ig heavy chain (su
38	431.5	69.9	123	2	A36006 Ig heavy chain V r
39	431	69.9	120	2	S31112 Ig heavy chain - h
40	431	69.9	122	2	S31675 Ig heavy chain V r
41	430.5	69.8	134	2	S31679 Ig heavy chain V r
42	430	69.7	122	2	S20772 Ig heavy chain V r
43	428.5	69.4	117	2	S78486 Ig heavy chain V r
44	428	69.4	122	2	S30533 Ig heavy chain V r
45	427.5	69.3	121	2	H36005 Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
S31107
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31107
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31107
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RAA>
A/Cross-references: EMBL:X62955
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          74.3%; Score 458.5; DB 2; Length 119;
Best Local Similarity 75.6%; Pred. No. 9.4e-34;
Matches 90; Conservative 7; Mismatches 19; Indels 3; Gaps 1;

Oy 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYHWRAQPGKLEWVARIDPANDITY 60
    |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWRQAPGKLEWVAISGSGSTYY 60
    |||||

Oy 61 ADSVKGRTTSSDSKRTAVYQNMSLRAEDTAVYYCT--ASGYWFAWGQGTLLTVSS 116
    |||||
Db 61 ADSVKGRTTSSDSKRTAVYQNMSLRAEDTAVYYCAKDPGASYFPDWGGTLLTVSS 119
    |||||

RESULT 2
S31109
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31109
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-117 <RAA>
A/Cross-references: EMBL:X62960
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-100/Domain: immunoglobulin homology <IMM>
```


QY 1 EVOLVESGGGLVOPGSSLRLSCAASGFNIKDTYIHMVROAPGKGLEWVARIDPANDNTIY 60
 Db 1 EVOLVESGGGVVOPGSSLRLSCAASGFTPDYTMHWROAPGKGLEWVSLISMDGSIY 60
 QY 61 ADSVKGRRFTISSDDSKNTAYLQWNSLRAPDTAVYCC---TASGYWPAWGGGTLYTVSS 116
 Db 61 ADSVKGRRFTISRDNKNSLYLQWNSLRTEDTALYYCAKDDSSGSYYFDYWGQGTLYTVSS 120

Search completed: May 13, 2004, 17:03:13
 Job time : 39.875 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:38:57 ; Search time 124.875 Seconds
(without alignments)
244.365 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566
Sequence: 1 DQMTQSPSSLSASVGRVT.....QQSNMPTFGQGTKEIKR 108

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	100.0	108	6	ABO27262
2	566	100.0	108	6	ABO27266
3	566	100.0	108	6	ABO27278
4	566	100.0	108	6	ABO27260
5	566	100.0	108	6	ABO27258
6	566	100.0	108	6	ABO27256
7	566	100.0	108	6	ABO27264
8	557	98.4	108	6	ABO27272
9	557	98.4	108	6	ABO27270
10	557	98.4	108	6	ABO27268
11	504	89.0	105	2	AAW87456
12	504	89.0	105	2	AAW87458
13	496	87.6	108	2	AAW70622
14	496	87.6	108	3	AAW82345
15	496	87.6	108	5	ABP61191
16	496	87.6	109	5	AAU74544
17	496	87.6	110	5	AAE28149
18	495	87.5	240	4	AAAB46010
19	495	87.5	240	4	AAAB45997
20	492	86.9	240	4	AAAB46001
21	491	86.7	107	4	AAAB62087
22	491	86.7	107	4	AAAB60400
23	491	86.7	107	4	AAAB61585
24	491	86.7	107	8	ADE71454
25	489	86.4	132	2	AAW22842

26	489	86.4	240	4	AAAB6004
27	488	86.2	108	6	ABP96009
28	488	86.2	240	2	AAV02472
29	488	86.2	240	4	AAAB5993
30	488	86.2	240	4	AAAB6040
31	488	86.2	240	4	AAAB6038
32	488	86.2	240	4	AAAB6008
33	488	86.2	240	4	AAAB6005
34	488	86.2	240	4	AAAB6005
35	488	86.2	240	6	ABP95997
36	487	86.0	236	5	AAU74297
37	487	86.0	240	4	AAAB6003
38	487	86.0	240	4	AAAB6048
39	485	85.7	256	3	AAV55072
40	485	85.7	367	3	AAV55078
41	485	85.7	546	3	AAV55074
42	485	85.7	626	3	AAV55081
43	484	85.5	107	2	AAV30770
44	484	85.5	109	2	AAV47041
45	484	85.5	109	2	AAV47041

ALIGNMENTS

RESULT 1 ✓
ABO27262 standard; protein; 108 AA.
ID ABO27262 standard; protein; 108 AA.
XX
AC ABO27262;
XX
DT 23-OCT-2003 (revised)
DT 11-SEP-2003 (first entry)
XX
DE ICM-1 binding humanised antibody Humd VL domain.
XX
KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KW respiratory syncytial virus; fungi; antibody; humanised antibody.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN US200305798-A1.
XX
PD 20-FEB-2003.
XX
PF 19-JUL-2001; 2001US-00910483. ✓
PR 30-NOV-1998; 98NO-US025422. ✓
PR 16-AUG-2000; 2000US-00555476. ✓
XX
PA (FANG/) FANG F.
PA (KOH/) KOHSTAEDT L.
PA (RENO/) RENO J.
XX
PI Fang F, Kohlstaedt L, Reno J;
XX
DR WPI; 2003-503356/47. —
XX
PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection
PT of cells expressing ICM-1, useful for treating infection caused by HRV,
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
XX protozoa.
PS Claim 1; Page 18; 30pp; English.
CC The invention relates to a humanised antibody that binds intracellular
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
CC expressing ICM-1, comprising any of the fully defined Huma to Humt
CC sequences. The methods and compositions are useful for inhibiting
CC infection and/or progression of infection caused by pathogens such as

CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)

XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 566; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2e-31;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSSSLASVGDVYITTCRASQSIINNLMHYQKPKAPKLIIYHASQISGVPS 60
 DB 1 DIQMTQSSSLASVGDVYITTCRASQSIINNLMHYQKPKAPKLIIYHASQISGVPS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCQNSNMPYTFGQGTVEIKR 108
 DB 61 RFSGSGSGTDFLTITSSLOPEDFATYYCQNSNMPYTFGQGTVEIKR 108

RESULT 2

ABO27266 ABO27266 standard; protein; 108 AA.

XX ABO27266;

DT 23-OCT-2003 (revised)
 DT 11-SEP-2003 (first entry)

DE ICAM-1 binding humanised antibody HumF vL domain.

KM Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
 KM human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.

OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.

XX US2003035798-A1.

XX 20-FEB-2003.

PF 19-JUL-2001; 2001US-00910483.

PR 30-NOV-1998; 98WO-US025422.

PR 16-AUG-2000; 2000US-00555446.

PA (FANG/) FANG F.
 PA (KOH/) KOHLSTADT L.
 PA (RENO/) RENO J.

PI Fang F, Kohlstaedt L, Reno J;

DR WPI; 2003-503356/47.

XX
 PT New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
 PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.

XX
 Claim 1; Page 19; 30pp; English.

XX The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humi
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 108 AA;

Query Match 100.0%; Score 566; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2e-31;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSSSLASVGDVYITTCRASQSIINNLMHYQKPKAPKLIIYHASQISGVPS 60
 DB 1 DIQMTQSSSLASVGDVYITTCRASQSIINNLMHYQKPKAPKLIIYHASQISGVPS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCQNSNMPYTFGQGTVEIKR 108
 DB 61 RFSGSGSGTDFLTITSSLOPEDFATYYCQNSNMPYTFGQGTVEIKR 108

RESULT 3

ABO27278 ABO27278 standard; protein; 108 AA.

XX ABO27278;

DT 23-OCT-2003 (revised)
 DT 11-SEP-2003 (first entry)

DE Humanised 1A6 (Hum19) antibody vL domain.

KM Human; mouse; 1A6; infection; human rhinovirus; human coxsackievirus;
 KM protozoa; malaria; respiratory syncytial virus; bacteria; fungi;
 KM humanised antibody; antibody.

OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.

XX US2003035798-A1.

XX 20-FEB-2003.

PF 19-JUL-2001; 2001US-00910483.

PR 30-NOV-1998; 98WO-US025422.

PR 16-AUG-2000; 2000US-00555446.

PA (FANG/) FANG F.
 PA (KOH/) KOHLSTADT L.
 PA (RENO/) RENO J.

PI Fang F, Kohlstaedt L, Reno J;

DR WPI; 2003-503356/47.

XX
 PT New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
 PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.

XX
 Example 2; Fig 3; 30pp; English.

XX The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humi
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of a humanised antibody 1A6 domain.
 CC (Updated on 23-OCT-2003 to standardise OS field)

XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 566; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2e-31;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVGDRTTTCRASQISNNLHMWYQKPKKLIYHASQISGVPS 60
 DB 1 DIQWTSPLSLASVGDRTTTCRASQISNNLHMWYQKPKKLIYHASQISGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQOSNSWPTYFGGTKEIKR 108
 DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQOSNSWPTYFGGTKEIKR 108

RESULT 4
 ABO27260 standard; protein; 108 AA.
 ID ABO27260;
 AC ABO27260;
 XX
 XX 23-OCT-2003 (revised)
 DT 11-SEP-2003 (first entry)
 DE ICAM-1 binding humanised antibody HumC vL domain.
 XX
 XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
 KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
 XX respiratory syncytial virus; fungi; antibody; humanised antibody.
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 OS
 OS US2003035798-A1.
 PN 20-FEB-2003.
 PD 19-JUL-2001; 2001US-00910483.
 XX
 XX 30-NOV-1998; 98WO-US025422.
 PR 16-AUG-2000; 2000US-00555446.
 XX
 XX (FANG/) FANG F.
 PA (KOH/L/) KOHLSTADT L.
 PA (RENO/) RENO J.
 PI Fang F, Kohlstaedt L, Reno J;
 XX
 XX WPI; 2003-503356/47.
 DR
 XX
 XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
 PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.
 XX
 XX Claim 1; Page 18; 30pp; English.
 PS
 XX The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
 CC expressing ICAM-1, comprising any of the fully defined HumC to HumL
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody
 CC domain. (Updated on 23-Oct-2003 to standardise OS field)
 CC
 XX
 XX Sequence 108 AA;
 SQ

Query Match 100.0%; Score 566; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2e-31;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVGDRTTTCRASQISNNLHMWYQKPKKLIYHASQISGVPS 60
 DB 1 DIQWTSPLSLASVGDRTTTCRASQISNNLHMWYQKPKKLIYHASQISGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQOSNSWPTYFGGTKEIKR 108
 DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQOSNSWPTYFGGTKEIKR 108

RESULT 5
 ABO27258 standard; protein; 108 AA.
 ID ABO27258;
 AC ABO27258;
 XX
 XX 23-OCT-2003 (revised)
 DT 11-SEP-2003 (first entry)
 DE ICAM-1 binding humanised antibody HumB vL domain.
 XX
 XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
 KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
 XX respiratory syncytial virus; fungi; antibody; humanised antibody.
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 OS
 OS US2003035798-A1.
 PN 20-FEB-2003.
 PD 19-JUL-2001; 2001US-00910483.
 XX
 XX 30-NOV-1998; 98WO-US025422.
 PR 16-AUG-2000; 2000US-00555446.
 XX
 XX (FANG/) FANG F.
 PA (KOH/L/) KOHLSTADT L.
 PA (RENO/) RENO J.
 PI Fang F, Kohlstaedt L, Reno J;
 XX
 XX WPI; 2003-503356/47.
 DR
 XX
 XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
 PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.
 XX
 XX Claim 1; Page 17; 30pp; English.
 PS
 XX The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
 CC expressing ICAM-1, comprising any of the fully defined HumA to HumL
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody
 CC domain. (Updated on 23-Oct-2003 to standardise OS field)
 CC
 XX
 XX Sequence 108 AA;
 SQ

Query Match 100.0%; Score 566; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2e-31;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVGDRTTTCRASQISNNLHMWYQKPKKLIYHASQISGVPS 60
 DB 1 DIQWTSPLSLASVGDRTTTCRASQISNNLHMWYQKPKKLIYHASQISGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQOSNSWPTYFGGTKEIKR 108
 DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQOSNSWPTYFGGTKEIKR 108

RESULT 6

ABO27256 standard; protein; 108 AA.

ABO27256;

23-OCT-2003 (revised)
11-SEP-2003 (first entry)

ICAM-1 binding humanised antibody Huma vL domain.

Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
respiratory syncytial virus; fungi; antibody; humanised antibody.Mus sp.
Homo sapiens.
Chimeric.

US2003035798-A1

20-FEB-2003.

19-JUL-2001; 2001US-00910483.

30-NOV-1998; 98WO-US025422.

16-AUG-2000; 2000US-00555446.

(FANG/) FANG F.
(KOH/) KOHLSTADT L.
(RENO/) RENO J.

Fang F, Kohlstaedt L, Reno J;

WPI; 2003-503356/47.

New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
of cells expressing ICAM-1, useful for treating infection caused by HRV,
coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
protozoa.

Claim 1; Page 17; 30pp; English.

The invention relates to a humanised antibody that binds intracellular
adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
expressing ICAM-1, comprising any of the fully defined Huma to Humt
sequences. The methods and compositions are useful for inhibiting
infection and/or progression of infection caused by pathogens such as
human rhinovirus, coxsackie A virus, respiratory syncytial virus,
bacteria, fungi and protozoa, in particular malaria. The present sequence
represents the amino acid sequence of ICAM-1 binding humanised antibody
domain. (Updated on 23-OCT-2003 to standardise OS field)

Sequence 108 AA;

Query Match 100.0%; Score 566; DB 6; Length 108;

Best Local Similarity 100.0%; Pred. No. 2e-31; Indels 0; Gaps 0;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKGKAPKLLIYHSAQSISGVPS 60

1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKGKAPKLLIYHSAQSISGVPS 60

61 RFSGSGSGTDFTLTISLQPEDPATYTCOQSNMPTTFGGGTVEIKR 108

61 RFSGSGSGTDFTLTISLQPEDPATYTCOQSNMPTTFGGGTVEIKR 108

ABO27264 standard; protein; 108 AA.

ABO27264;

AC ABO27264;

23-OCT-2003 (revised)

11-SEP-2003 (first entry)

ICAM-1 binding humanised antibody Hume vL domain.

Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
respiratory syncytial virus; fungi; antibody; humanised antibody.Mus sp.
Homo sapiens.
Chimeric.

US2003035798-A1

20-FEB-2003.

19-JUL-2001; 2001US-00910483.

30-NOV-1998; 98WO-US025422.

16-AUG-2000; 2000US-00555446.

(FANG/) FANG F.
(KOH/) KOHLSTADT L.
(RENO/) RENO J.

Fang F, Kohlstaedt L, Reno J;

WPI; 2003-503356/47.

New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
of cells expressing ICAM-1, useful for treating infection caused by HRV,
coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
protozoa.

Claim 1; Page 18-19; 30pp; English.

The invention relates to a humanised antibody that binds intracellular
adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
expressing ICAM-1, comprising any of the fully defined Huma to Humt
sequences. The methods and compositions are useful for inhibiting
infection and/or progression of infection caused by pathogens such as
human rhinovirus, coxsackie A virus, respiratory syncytial virus,
bacteria, fungi and protozoa, in particular malaria. The present sequence
represents the amino acid sequence of ICAM-1 binding humanised antibody
domain. (Updated on 23-OCT-2003 to standardise OS field)

Sequence 108 AA;

Query Match 100.0%; Score 566; DB 6; Length 108;

Best Local Similarity 100.0%; Pred. No. 2e-31; Indels 0; Gaps 0;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKGKAPKLLIYHSAQSISGVPS 60

1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKGKAPKLLIYHSAQSISGVPS 60

61 RFSGSGSGTDFTLTISLQPEDPATYTCOQSNMPTTFGGGTVEIKR 108

61 RFSGSGSGTDFTLTISLQPEDPATYTCOQSNMPTTFGGGTVEIKR 108

ABO27272 standard; protein; 108 AA.

ABO27272;

AC ABO27272;

23-OCT-2003 (revised)

11-SEP-2003 (first entry)

ICAM-1 binding humanised antibody Humi vL domain.

XX Human: mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KM respiratory syncytial virus; fungi; antibody; humanised antibody.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
XX US2003035798-A1.
XX PD 20-FEB-2003.
XX PF 19-JUL-2001; 2001US-00910483.
XX PR 30-NOV-1998; 98WO-US025422.
XX PR 16-AUG-2000; 2000US-00555446.
XX
XX (FANG/) FANG F.
XX (KOH/) KOHLSTADT L.
XX (RENO/) RENO J.
XX
XX Fang F, Kohlstaedt L, Reno J;
XX WPI; 2003-503356/47.
XX
XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.
XX
XX Claim 1; Page 20; 30pp; English.
XX
XX The invention relates to a humanised antibody that binds intracellular
CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
CC expressing ICAM-1, comprising any of the fully defined Huma to Humt
CC sequences. The methods and compositions are useful for inhibiting
CC infection and/or progression of infection caused by pathogens such as
CC human rhinovirus, coxackie A virus, respiratory syncytial virus,
CC bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICAM-1 binding humanised antibody
CC domain. (Updated on 23-Oct-2003 to standardise OS field)
XX
XX Sequence 108 AA;
SQ
Query Match 98.4%; Score 557; DB 6; Length 108;
Best Local Similarity 99.1%; Pred. No. 8e-31;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVITTCRASQISINNLHWYQOKGKAPKLLIYASQISIGVPS 60
DB 1 DIQMTQSPSSLSASVGRVITTCRASQISINNLHWYQOKGKAPKLLIYASQISIGVPS 60
QY 61 RFGSGSGGTDFLTITISLQPEDFATYVCCQSNMWPYFGGQTKVEIKR 108
DB 61 RFGSGSGGTDFLTITISLQPEDFATYVCCQSNMWPYFGGQTKVEIKR 108
RESULT 9
ID ABO27270 standard; protein: 108 AA.
XX ABO27270;
XX
XX 23-OCT-2003 (revised)
XX 11-SEP-2003 (first entry)
XX
XX ICAM-1 binding humanised antibody HumH VL domain.
XX
XX Human: mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KM respiratory syncytial virus; fungi; antibody; humanised antibody.
XX

OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
XX US2003035798-A1.
XX PD 20-FEB-2003.
XX PF 19-JUL-2001; 2001US-00910483.
XX PR 30-NOV-1998; 98WO-US025422.
XX PR 16-AUG-2000; 2000US-00555446.
XX
XX (FANG/) FANG F.
XX (KOH/) KOHLSTADT L.
XX (RENO/) RENO J.
XX
XX Fang F, Kohlstaedt L, Reno J;
XX WPI; 2003-503356/47.
XX
XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.
XX
XX Claim 1; Page 20; 30pp; English.
XX
XX The invention relates to a humanised antibody that binds intracellular
CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
CC expressing ICAM-1, comprising any of the fully defined Huma to Humt
CC sequences. The methods and compositions are useful for inhibiting
CC infection and/or progression of infection caused by pathogens such as
CC human rhinovirus, coxackie A virus, respiratory syncytial virus,
CC bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICAM-1 binding humanised antibody
CC domain. (Updated on 23-Oct-2003 to standardise OS field)
XX
XX Sequence 108 AA;
SQ
Query Match 98.4%; Score 557; DB 6; Length 108;
Best Local Similarity 99.1%; Pred. No. 8e-31;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVITTCRASQISINNLHWYQOKGKAPKLLIYASQISIGVPS 60
DB 1 DIQMTQSPSSLSASVGRVITTCRASQISINNLHWYQOKGKAPKLLIYASQISIGVPS 60
QY 61 RFGSGSGGTDFLTITISLQPEDFATYVCCQSNMWPYFGGQTKVEIKR 108
DB 61 RFGSGSGGTDFLTITISLQPEDFATYVCCQSNMWPYFGGQTKVEIKR 108
RESULT 10
ID ABO27268 standard; protein: 108 AA.
XX ABO27268;
XX
XX 23-OCT-2003 (revised)
XX 11-SEP-2003 (first entry)
XX
XX ICAM-1 binding humanised antibody HumH VL domain.
XX
XX Human: mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KM respiratory syncytial virus; fungi; antibody; humanised antibody.
XX
XX Mus sp.
XX Homo sapiens.
XX Chimeric.
XX US2003035798-A1.

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XX 20-FEB-2003.
XX
XX 19-JUL-2001; 2001US-00910483.
XX
XX 30-NOV-1998; 98WO-US025422.
XX
XX 16-AUG-2000; 2000US-00555446.
XX
XX (FANG/) FANG F.
XX (KOH/) KOHLSTADT L.
XX (RENO/) RENO J.
XX
XX Fang F, Kohlstaedt L, Reno J;
XX
XX WPI; 2003-503356/47.
XX
XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
XX of cells expressing ICAM-1, useful for treating infection caused by HRV,
XX PT Coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
XX PT protozoa.
XX
XX Claim 1; Page 19; 30pp; English.
XX
XX The invention relates to a humanised antibody that binds intracellular
XX adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
XX expressing ICAM-1, comprising any of the fully defined Huma to Humi
XX CC sequences. The methods and compositions are useful for inhibiting
XX CC infection and/or progression of infection caused by pathogens such as
XX human rhinovirus, coxsackie A virus, respiratory syncytial virus,
XX bacteria, fungi and protozoa, in particular malaria. The present sequence
XX CC represents the amino acid sequence of ICAM-1 binding humanised antibody
XX domain. (Updated on 23-Oct-2003 to standardise OS field)
XX
XX Sequence 108 AA;
XX
XX Query Match 98.4%; Score 557; DB 6; Length 108;
XX Best Local Similarity 99.1%; Pred. No. 8e-31;
XX Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 DIOMTQSPSLASVGDRTVITTCRASQISNNLHWYQKRGKAPKLLIYHSAQSIGVPS 60
XX 1 DIOMTQSPSLASVGDRTVITTCRASQISNNLHWYQKRGKAPKLLIYHSAQSIGVPS 60
XX
XX 61 RFGSGSGGTDFTLTISLQPEDPATYTCQOSNSWPYTFGQGTVEIKR 108
XX 61 RFGSGSGGTDFTLTISLQPEDPATYTCQOSNSWPYTFGQGTVEIKR 108
XX
XX Db 61 RFGSGSGGTDFTLTISLQPEDPATYTCQOSNSWPYTFGQGTVEIKR 108
XX
XX RESULT 11
XX AAM87456
XX ID AAM87456 standard; protein; 105 AA.
XX
XX AAM87456;
XX
XX 15-MAR-1999 (first entry)
XX
XX Jk gene product.
XX
XX Humanised antibody; monoclonal antibody; Mab; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;
XX metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis;
XX diabetic retinopathy; inflammation; macular degeneration; osteoporosis;
XX Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;
XX immunotherapy; D12HZREI; Jk protein.
XX
XX Mus sp.
XX
XX OS
XX PN WO9840488-A1.
XX
XX PD 17-SEP-1998.
XX
XX PF 12-MAR-1998; 98WO-US004987.
XX
XX DR

```

```

PR 12-MAR-1997; 97US-0039609P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Jonak ZL, Johanson KO, Taylor AH;
XX
XX WPI; 1999-034590/03.
XX
XX N-PSDB; AAV71803.
XX
XX New anti alpha v beta 3 vitronectin receptor antibodies - used for
XX PT immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory
XX PT disorders, atherosclerosis, restenosis, cancers or osteoporosis.
XX
XX Example 14; Page 66; 97pp; English.
XX
XX This polypeptide is encoded by a Jk synthetic gene segment (see
XX CC AAV71803). It was utilising in novel D12HZREI humanised light chain
XX CC variable region (see AAM87458), which comprises a human REI framework and
XX CC complementary determining regions from the anti-human alpha-v beta-3
XX CC vitronectin receptor monoclonal antibody D12. Humanised D12 antibodies
XX CC can be used for passive immunotherapy of disorders mediated by the alpha-
XX CC v beta-3 vitronectin receptor, e.g. restenosis and angiogenic associated
XX CC diseases
XX
XX Sequence 105 AA;
XX
XX Query Match 89.0%; Score 504; DB 2; Length 105;
XX Best Local Similarity 90.5%; Pred. No. 3.1e-27;
XX Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 DIOMTQSPSLASVGDRTVITTCRASQISNNLHWYQKRGKAPKLLIYHSAQSIGVPS 60
XX 1 DIVLTQSPSLASVGDRTVITTCRASQISNNLHWYQKRGKAPKLLIYHSAQSIGVPS 60
XX
XX 61 RFGSGSGGTDFTLTISLQPEDPATYTCQOSNSWPYTFGQGTVEIKR 105
XX 61 RFGSGSGGTDFTLTISLQPEDPATYTCQOSNSWPYTFGQGTVEIKR 105
XX
XX Db 61 RFGSGSGGTDFTLTISLQPEDPATYTCQOSNSWPYTFGQGTVEIKR 105
XX
XX RESULT 12
XX AAM87458
XX ID AAM87458 standard; protein; 105 AA.
XX
XX AAM87458;
XX
XX 15-MAR-1999 (first entry)
XX
XX Humanised anti-alpha-v beta-3 Mab D12HZLCREI VL.
XX
XX Humanised antibody; monoclonal antibody; Mab; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;
XX metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis;
XX diabetic retinopathy; inflammation; macular degeneration; osteoporosis;
XX Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;
XX immunotherapy; D12HZLCREI.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9840488-A1.
XX
XX PD 17-SEP-1998.
XX
XX PF 12-MAR-1998; 98WO-US004987.
XX
XX PR 12-MAR-1997; 97US-0039609P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Jonak ZL, Johanson KO, Taylor AH;
XX
XX WPI; 1999-034590/03.
XX
XX N-PSDB; AAV71805.
XX
XX DR

```

XX New anti alpha v beta 3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory
PT disorders, atherosclerosis, restenosis, cancers or osteoporosis.

XX Example 14; Page 68-69; 97pp; English.

XX This is the amino acid sequence of the light chain variable region (VL)
CC of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody
CC D12H2C2RE1. It is based on a synthetic humanised kappa chain based on a
CC modified human KBI kappa framework and complementarity determining
CC regions from the murine anti-human alpha-v beta-3 vitronectin receptor
CC monoclonal antibody D12 (see AAW84094). Humanised antibodies of the
CC invention can be used for passive immunotherapy of a disorder mediated by
CC the alpha-v beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
CC related disorders, such as angiogenesis associated with diabetic
CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
CC disorders, macular degeneration, rheumatoid arthritis and cancer, e.g.
CC solid tumour metastasis, and diseases where bone resorption is associated
CC with pathology such as osteoporosis, hyperparathyroidism, Paget's
CC disease, hypercalcaemia of malignancy, osteolytic lesions produced by bone
CC metastasis, bone loss due to immobilisation or sex hormone deficiency.
CC They can also be used for targeted drug therapy, and for detection and
CC diagnosis

XX Sequence 105 AA;

Query Match 89.0%; Score 504; DB 2; Length 105;
Best Local Similarity 90.5%; Pred. No. 3.1e-27;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCRASQSSINNTLMHYQKPKAPKLLIYHASSISGVPS 60
DB 1 DIVIQSPSSLSASVGDRTVITTCRASQSSINNTLMHYQKPKAPKLLIYHASSISGVPS 60
QY 61 RFGSGSGGTDFTLTSSLOPEDFATYYCOQSNMPTFGQGTKEIR 105
DB 61 RFGSGSGGTDFTLTSSLOPEDFATYYCOQSNMPTFGQGTKEIR 105

RESULT 13
AAW70622
ID AAW70622 standard; peptide; 108 AA.

XX AC AAW70622;

XX DT 27-JAN-1999 (first entry)

XX DE Human consensus framework hum kappa1 for light kappa subgroup 1.

XX Light variable domain; murine; humanised antibody;
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX VEGF-induced angiogenesis; tumour; retinal disorder;
XX age-related macular degeneration; diabetic retinopathy;
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease;
XX Human consensus framework hum kappa1; light kappa subgroup 1.

XX OS Homo sapiens.

XX PN MO9845331-A2.

XX PD 15-OCT-1998.

XX PF 03-APR-1998; 98WO-US0006604.

XX PR 07-APR-1997; 97US-00833504.

XX PR 06-AUG-1997; 97US-00908469.

XX PA (GETH) GENENTECH INC.

XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT sites, also related nucleic acid, vectors and transformed cells.

XX Example 1; Fig 1B; 100pp; English.

XX The present sequence represents the human consensus framework hum kappa1
CC for light kappa subgroup 1. The sequence is used to humanise the variable
CC light domain of the murine anti-vascular endothelial growth factor (anti-
CC VEGF) antibody A4.6.1. The humanised antibodies are used to inhibit VEGF
CC -induced angiogenesis, particularly for treating or preventing tumours
CC (of any type) and retinal disorders (e.g. age-related macular
CC degeneration or diabetic retinopathy). They can also be used to treat
CC other conditions that involve angiogenesis, e.g. rheumatoid arthritis,
CC psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 108 AA;

Query Match 87.6%; Score 496; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 1.1e-26;
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCRASQSSINNTLMHYQKPKAPKLLIYHASSISGVPS 60
DB 1 DIVIQSPSSLSASVGDRTVITTCRASQSSINNTLMHYQKPKAPKLLIYHASSISGVPS 60
QY 61 RFGSGSGGTDFTLTSSLOPEDFATYYCOQSNMPTFGQGTKEIR 108
DB 61 RFGSGSGGTDFTLTSSLOPEDFATYYCOQSNMPTFGQGTKEIR 108

RESULT 14
AAW82345
ID AAW82345 standard; protein; 108 AA.

XX AC AAW82345;

XX DT 22-JUN-2000 (first entry)

XX DE Human consensus sequence of light chain subgroup KI SEQ ID NO:3.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
XX antitumour; antiviral; inflammation; immunological response; LPA-1;
XX lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
XX inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
XX viral infection; transplant rejection; graft rejection.

XX OS Homo sapiens.

XX PN US6037454-A.

XX PD 14-MAR-2000.

XX PF 20-NOV-1997; 97US-00974899.

XX PR 27-NOV-1996; 96US-0031971P.

XX PA (GETH) GENENTECH INC.

XX PI Jardieu PM, Presta LG;

XX WPI; 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.
PT inflammation and transplant rejection, contains human heavy variable
PT region complementarity determining regions.

XX Example; Fig 1; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that
CC binds specifically to the human CD11a I-domain. The Ab has anti-
CC inflammatory, immunosuppressant, antitumour and antiviral activities. The

CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of a humanised antibody 1A6 domain.
 CC (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 116 AA;

Query Match 100.0%; Score 617; DB 6; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2,1e-47;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGFRFTISSDSSKNTAVLQNNSLRAEDTAVYYCTASGYWPAWVGQGLVTYSS 116
 DB 61 ADSVKGFRFTISSDSSKNTAVLQNNSLRAEDTAVYYCTASGYWPAWVGQGLVTYSS 116

RESULT 2

ABO27257 standard; protein; 116 AA.

AC ABO27257;
 DT 23-OCT-2003 (revised)
 DT 11-SEP-2003 (first entry)

DE ICM-1 binding humanised antibody HumB vH domain.

KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;
 KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
 KW respiratory syncytial virus; fungi; antibody; humanised antibody.

OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.

PN US2003035798-A1.

PD 20-FEB-2003.

PF 19-JUL-2001; 2001US-00910483.

PR 30-NOV-1998; 98WO-US025422.

PR 16-AUG-2000; 2000US-00555446.

PA (FANG/) FANG F.
 PA (KOHL/) KOHLSTADT L.

PA (RENO/) RENO J.

PI Fang F, Kohlstaedt L, Reno J;

WPI; 2003-503356/47.

PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection
 PT of cells expressing ICM-1, useful for treating infection caused by HRV,
 PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.

PS Claim 1; Page 17; 30pp; English.

CC The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
 CC expressing ICM-1, comprising any of the fully defined HumA to HumI
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICM-1 binding humanised antibody
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 116 AA;

Query Match 100.0%; Score 617; DB 6; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2,1e-47;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGFRFTISSDSSKNTAVLQNNSLRAEDTAVYYCTASGYWPAWVGQGLVTYSS 116
 DB 61 ADSVKGFRFTISSDSSKNTAVLQNNSLRAEDTAVYYCTASGYWPAWVGQGLVTYSS 116

RESULT 3

ABO27261 standard; protein; 116 AA.

AC ABO27261;

DT 23-OCT-2003 (revised)
 DT 11-SEP-2003 (first entry)

DE ICM-1 binding humanised antibody HumB vH domain.

KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;
 KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
 KW respiratory syncytial virus; fungi; antibody; humanised antibody.

OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.

PN US2003035798-A1.

PD 20-FEB-2003.

PF 19-JUL-2001; 2001US-00910483.

PR 30-NOV-1998; 98WO-US025422.

PR 16-AUG-2000; 2000US-00555446.

PA (FANG/) FANG F.
 PA (KOHL/) KOHLSTADT L.

PA (RENO/) RENO J.

PI Fang F, Kohlstaedt L, Reno J;

WPI; 2003-503356/47.

PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection
 PT of cells expressing ICM-1, useful for treating infection caused by HRV,
 PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.

PS Claim 1; Page 18; 30pp; English.

CC The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
 CC expressing ICM-1, comprising any of the fully defined HumA to HumI
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICM-1 binding humanised antibody
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 116 AA;

Query Match 99.4%; Score 613; DB 6; Length 116;
 Best Local Similarity 99.1%; Pred. No. 4,8e-47;
 Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGIVOPGGSLRLSCAASGFINIKDTYIHWROAPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGIVOPGGSLRLSCAASGFINIKDTYIHWROAPGKLEWVARIDPANDNTIY 60
QY 61 ADSVKGKFTTSSDPSKNTATYLOMNSLRAPDTAVYYCTASGYWFAWMGQGLTVTVSS 116
DB 61 ADSVKGKFTTSSDPSKNTATYLOMNSLRAPDTAVYYCTTSGYWFAYMGQGLTVTVSS 116

RESULT 4

ABO27255 standard; protein; 116 AA.

AC ABO27255;
XX
XX 23-OCT-2003 (revised)
DT 11-SEP-2003 (first entry)
XX
XX ICM-1 binding humanised antibody Huma VH domain.
DE
XX Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KW respiratory syncytial virus; fungi; antibody; humanised antibody.
XX

OS Mus sp.
OS Homo sapiens.
OS Chimeric.

XX US2003035798-A1.

XX 20-FEB-2003.

XX 19-JUL-2001; 2001US-00910483.

XX 30-NOV-1998; 98WO-US025422.

XX 16-AUG-2000; 2000US-00555446.

XX (FANG/) FANG F.
XX (KOH/) KOHLSTAEDT L.
XX (RENO/) RENO J.

XX Fang F, Kohlstaedt L, Reno J;

XX WPI; 2003-503356/47.

XX New humanized antibody binding ICM-1 and/or inhibits pathogen infection
PT of cells expressing ICM-1, useful for treating infection caused by HRV,
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.

XX Claim 1; Page 17; 30pp; English.

XX The invention relates to a humanised antibody that binds intracellular
adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
expressing ICM-1, comprising any of the fully defined Huma to Humt
sequences. The methods and compositions are useful for inhibiting
infection and/or progression of infection caused by pathogens such as
human rhinovirus, coxsackie A virus, respiratory syncytial virus,
bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICM-1 binding humanised antibody
domain. (Updated on 23-Oct-2003 to standardise OS field)

XX Sequence 116 AA;

Query Match 99.0%; Score 611; DB 6; Length 116;

Best Local Similarity 99.1%; Pred. No. 7.3e-47;

Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGIVOPGGSLRLSCAASGFINIKDTYIHWROAPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGIVOPGGSLRLSCAASGFINIKDTYIHWROAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGKFTTSSDPSKNTATYLOMNSLRAPDTAVYYCTASGYWFAWMGQGLTVTVSS 116
DB 61 ADSVKGKFTTSSDPSKNTATYLOMNSLRAPDTAVYYCTDSGYWFAYMGQGLTVTVSS 116

RESULT 5

ABO27267 standard; protein; 116 AA.

XX ABO27267;

XX 23-OCT-2003 (revised)

DT 11-SEP-2003 (first entry)

XX

XX ICM-1 binding humanised antibody Huma VH domain.

DE Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;

KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;

KW respiratory syncytial virus; fungi; antibody; humanised antibody.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

XX US2003035798-A1.

XX 20-FEB-2003.

XX 19-JUL-2001; 2001US-00910483.

XX 30-NOV-1998; 98WO-US025422.

XX 16-AUG-2000; 2000US-00555446.

XX (FANG/) FANG F.
XX (KOH/) KOHLSTAEDT L.
XX (RENO/) RENO J.

XX Fang F, Kohlstaedt L, Reno J;

XX WPI; 2003-503356/47.

XX New humanized antibody binding ICM-1 and/or inhibits pathogen infection
PT of cells expressing ICM-1, useful for treating infection caused by HRV,
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.

XX Claim 1; Page 19; 30pp; English.

XX The invention relates to a humanised antibody that binds intracellular
adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
expressing ICM-1, comprising any of the fully defined Huma to Humt
sequences. The methods and compositions are useful for inhibiting
infection and/or progression of infection caused by pathogens such as
human rhinovirus, coxsackie A virus, respiratory syncytial virus,
bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICM-1 binding humanised antibody
domain. (Updated on 23-Oct-2003 to standardise OS field)

XX Sequence 116 AA;

Query Match 98.9%; Score 610; DB 6; Length 116;

Best Local Similarity 98.3%; Pred. No. 8.9e-47;

Matches 114; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGIVOPGGSLRLSCAASGFINIKDTYIHWROAPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGIVOPGGSLRLSCAASGFINIKDTYIHWROAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGKFTTSSDPSKNTATYLOMNSLRAPDTAVYYCTASGYWFAWMGQGLTVTVSS 116
DB 61 ADSVKGKFTTSSDPSKNTATYLOMNSLRAPDTAVYYCTTSGYWFAYMGQGLTVTVSS 116

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RESULT 6
ABO27259
ID ABO27259 standard; protein; 116 AA.
XX
AC ABO27259;
XX
DT 23-OCT-2003 (revised)
DT 11-SEP-2003 (first entry)
XX
DE ICM-1 binding humanised antibody Humc VH domain.
XX
KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KW respiratory syncytial virus; fungi; antibody; humanised antibody.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FN US2003035798-A1.
XX
PD 20-FEB-2003.
XX
PF 19-JUL-2001; 2001US-00910483.
XX
PR 30-NOV-1998; 98WO-US025422.
PR 16-AUG-2000; 2000US-0055446.
XX
PA (FANG/) FANG F.
PA (KOH/) KOHLSTAEDE L.
PA (RENO/) RENO J.
XX
PI Fang F, Kohlstaedt L, Reno J;
XX
DR WPI; 2003-503356/47.
XX
PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection
PT of cells expressing ICM-1, useful for treating infection caused by HRV,
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.
XX
PS Claim 1; Page 18; 30pp; English.
XX
CC The invention relates to a humanised antibody that binds intracellular
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
CC expressing ICM-1, comprising any of the fully defined Huma to Humt
CC sequences. The methods and compositions are useful for inhibiting
CC infection and/or progression of infection caused by pathogens such as
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
CC bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICM-1 binding humanised antibody
CC domain. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 116 AA;
XX
Query Match 98.7%; Score 609; DB 6; Length 116;
Best Local Similarity 98.3%; Pred. No. 1,1e-46;
Matches 114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 EVOLVESGGGLVOPGSGSLRISCAASGFNIKDTYIHWVRQAPGKLEWVARIDPANDNTIY 60
Db 1 EVOLVESGGGLVOPGSGSLRISCAASGFNIKDTYIHWVRQAPGKLEWVARIDPANDNTIY 60
XX
QY 61 ADVSKGRFTTISDSDSKNTAYLQMSLRAEDTAIVVYCTSGYFAWGGTLVTYSS 116
Db 61 ADVSKGRFTTISDSDSKNTAYLQMSLRAEDTAIVVYCTSGYFAWGGTLVTYSS 116
XX
RESULT 7
ABO27265
ID ABO27265 standard; protein; 117 AA.
XX
AC ABO27265;

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XX
DT 23-OCT-2003 (revised)
DT 11-SEP-2003 (first entry)
XX
DE ICM-1 binding humanised antibody Humf VH domain.
XX
KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KW respiratory syncytial virus; fungi; antibody; humanised antibody.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FN US2003035798-A1.
XX
PD 20-FEB-2003.
XX
PF 19-JUL-2001; 2001US-00910483.
XX
PR 30-NOV-1998; 98WO-US025422.
PR 16-AUG-2000; 2000US-0055446.
XX
PA (FANG/) FANG F.
PA (KOH/) KOHLSTAEDE L.
PA (RENO/) RENO J.
XX
PI Fang F, Kohlstaedt L, Reno J;
XX
DR WPI; 2003-503356/47.
XX
PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection
PT of cells expressing ICM-1, useful for treating infection caused by HRV,
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.
XX
PS Claim 1; Page 19; 30pp; English.
XX
CC The invention relates to a humanised antibody that binds intracellular
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
CC expressing ICM-1, comprising any of the fully defined Huma to Humt
CC sequences. The methods and compositions are useful for inhibiting
CC infection and/or progression of infection caused by pathogens such as
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
CC bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICM-1 binding humanised antibody
CC domain. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 117 AA;
XX
Query Match 97.2%; Score 599.5; DB 6; Length 117;
Best Local Similarity 97.4%; Pred. No. 7,8e-46;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
XX
QY 1 EVOLVESGGGLVOPGSGSLRISCAASGFNIKDTYIHWVRQAPGKLEWVARIDPANDNTI 59
Db 1 EVOLVESGGGLVOPGSGSLRISCAASGFNIKDTYIHWVRQAPGKLEWVARIDPANDNTI 60
XX
QY 60 YADVSKGRFTTISDSDSKNTAYLQMSLRAEDTAIVVYCTSGYFAWGGTLVTYSS 116
Db 61 YADVSKGRFTTISDSDSKNTAYLQMSLRAEDTAIVVYCTSGYFAWGGTLVTYSS 117
XX
RESULT 8
ABO27269
ID ABO27269 standard; protein; 116 AA.
XX
AC ABO27269;
XX
DT 23-OCT-2003 (revised)
DT 11-SEP-2003 (first entry)
XX
DE ICM-1 binding humanised antibody Humh VH domain.

```

XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
 KM human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX US2003035798-A1.
 XX 20-FEB-2003.
 XX 19-JUL-2001; 2001US-00910483.
 PF 30-NOV-1998; 98MO-US025422.
 PR 16-AUG-2000; 2000US-00555446.
 XX (FANG/) FANG F.
 PA (KOH/) KOHLSTAEDT L.
 PA (RENO/) RENO J.
 PI Fang F, Kohlstaedt L, Reno J;
 PI WPI; 2003-503356/47.
 DR New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
 PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.
 PS Claim 1; Page 19; 30pp; English.
 XX The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humi
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)
 XX
 SO Sequence 116 AA;
 Query Match 95.5%; Score 589; DB 6; Length 116;
 Best Local Similarity 94.8%; Pred. No. 6.6e-45;
 Matches 110; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60
 DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60
 QY 61 ADSYKGRFTISDDSKNTAYLQNNSLRAEDTAVYYCTASGYWPAWVGGLVTYSS 116
 DB 61 DPKYQGRFTISADSKNTAYLQNNSLRAEDTAVYYCTTSGWFWPAWVGGLVTYSS 116
 Db 61 DPKYQGRFTISADSKNTAYLQNNSLRAEDTAVYYCTTSGWFWPAWVGGLVTYSS 116
 RESULT 9
 ABO27263 ID ABO27263 standard; protein; 116 AA.
 XX ABO27263;
 AC ABO27263;
 XX 23-OCT-2003 (revised)
 DT 11-SEP-2003 (first entry)
 XX ICM-1 binding humanised antibody Hume VH domain.
 DE Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
 KM human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.
 XX

OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX US2003035798-A1.
 XX 20-FEB-2003.
 XX 19-JUL-2001; 2001US-00910483.
 PF 30-NOV-1998; 98MO-US025422.
 PR 16-AUG-2000; 2000US-00555446.
 XX (FANG/) FANG F.
 PA (KOH/) KOHLSTAEDT L.
 PA (RENO/) RENO J.
 PI Fang F, Kohlstaedt L, Reno J;
 PI WPI; 2003-503356/47.
 DR New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
 PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.
 PS Claim 1; Page 18; 30pp; English.
 XX The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humi
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)
 XX
 SO Sequence 116 AA;
 Query Match 95.5%; Score 589; DB 6; Length 116;
 Best Local Similarity 94.8%; Pred. No. 6.6e-45;
 Matches 110; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60
 DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60
 QY 61 ADSYKGRFTISDDSKNTAYLQNNSLRAEDTAVYYCTASGYWPAWVGGLVTYSS 116
 DB 61 DPKYQGRFTISADSKNTAYLQNNSLRAEDTAVYYCTTSGWFWPAWVGGLVTYSS 116
 Db 61 DPKYQGRFTISADSKNTAYLQNNSLRAEDTAVYYCTTSGWFWPAWVGGLVTYSS 116
 RESULT 10
 ABO27271 ID ABO27271 standard; protein; 116 AA.
 XX ABO27271;
 AC ABO27271;
 XX 23-OCT-2003 (revised)
 DT 11-SEP-2003 (first entry)
 XX ICM-1 binding humanised antibody Humi VH domain.
 DE Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;
 KM human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.
 XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX US2003035798-A1.
 XX

XX 20-FEB-2003.
 XX
 XX 19-JUN-2001; 2001US-00910483.
 XX
 XX 30-NOV-1998; 98WO-US025422.
 XX 16-AUG-2000; 2000US-00555446.
 XX
 XX (FANG/) FANG F.
 XX (KOH/) KOHLSTADT L.
 XX (RENO/) RENO J.
 XX
 XX Fang F, Kohlstaedt L, Reno J;
 XX WPI; 2003-503356/47.
 XX
 XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
 PT of cells expressing ICAM-1, useful for treating infection caused by HIV,
 PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and
 PT protozoa.
 XX
 XX Claim 1; Page 20; 30pp; English.
 XX
 CC The invention relates to a humanised antibody that binds intracellular
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humt
 CC sequences. The methods and compositions are useful for inhibiting
 CC infection and/or progression of infection caused by pathogens such as
 CC human rhinovirus, coxackie A virus, respiratory syncytial virus,
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)
 XX
 XX Sequence 116 AA;

Query Match 93.4%; Score 576; DB 6; Length 116;
 Best Local Similarity 92.2%; Pred. No. 9.5e-44;
 Matches 107; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGFRNIKDTYIHWVRQAPGKGLIEWVARIDPANDNTIY 60
 DB 1 EVOLVESGGGLVPGGSLRLSCAASGFRNIKDTYIHWVRQAPGKGLIEWVARIDPANDNTIY 60
 QY 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRAPDTAVYYCTASGTFWPAWVGQGLTVTVSS 116
 DB 61 DPKYQGRFTMSADTSKNTAYLQWNSLRAPDTAVYYCTTSGWFWPAWVGQGLTVTVSS 116

RESULT 11
 ABR55857
 ID ABR55857 standard; protein; 120 AA.
 AC ABR55857;

XX 02-SEP-2003 (first entry)
 DT
 XX
 XX Anti-Her-2 Mab herceptin heavy chain.
 DE
 XX
 KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
 KW antibody; Her-2; epidermal growth factor receptor.
 XX
 XX Mus musculus.
 OS
 XX
 XX WO2003031464-A2.
 XX
 XX 17-APR-2003.
 PD
 XX
 XX 09-OCT-2002; 2002WO-US032263.
 PF
 XX
 XX 10-OCT-2001; 2001US-0328523P.
 PR 19-OCT-2001; 2001US-0344692P.
 PR 28-NOV-2001; 2001US-0334233P.
 PR 28-NOV-2001; 2001US-0334301P.

PR 07-JUN-2002; 2002US-0387292P.
 PR 25-JUN-2002; 2002US-0391777P.
 PR 17-JUN-2002; 2002US-0396594P.
 PR 16-AUG-2002; 2002US-0404249P.
 PR 28-AUG-2002; 2002US-0407527P.
 XX
 XX (NEOS-) NEOSE TECHNOLOGIES INC.
 XX
 XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
 XX WPI; 2003-449162/42.
 XX
 XX Remodeling a peptide, by removing a saccharyl subunit from the peptide to
 PT form truncated glycan, and adding or deleting glycosyl groups to a
 PT peptide and/or adding modifying group of a peptide to remodel the
 PT peptide.
 XX
 XX Example; Fig 72B; 900pp; English.

XX The invention relates to a cell-free, in vitro method of remodeling a
 CC peptide. The method involves removing a saccharyl subunit from the
 CC peptide, thus forming a truncated glycan, and contacting the truncated
 CC glycan with at least one glycosyltransferase and at least one glycosyl
 CC donor under conditions suitable to transfer at least one glycosyl donor
 CC to the truncated glycan, thus remodeling the peptide. Conjugates can be
 CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,
 CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
 CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
 CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
 CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-P1)
 CC peptide, beta-glucosidase peptide, tissue plasminogen activator (tPA)
 CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
 CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
 CC glycoprotein iib/iriia monoclonal antibody peptide, chimeric anti-HER2
 CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
 CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
 CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth
 CC hormone (HGH) peptide, and a modifying group, where the modifying group
 CC is covalently attached to the peptide through an intact glycosyl linking
 CC group. The method is useful for a cell-free, in vitro method of
 CC remodeling the above mentioned peptides. The present sequence represents
 CC an anti-Her-2 (human epidermal growth factor receptor) Mab herceptin
 CC heavy chain
 XX

QY Sequence 120 AA;
 SO
 Query Match 84.0%; Score 518; DB 6; Length 120;
 Best Local Similarity 85.8%; Pred. No. 1.4e-38;
 Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGFRNIKDTYIHWVRQAPGKGLIEWVARIDPANDNTIY 60
 DB 1 EVOLVESGGGLVPGGSLRLSCAASGFRNIKDTYIHWVRQAPGKGLIEWVARIDPANDNTIY 60
 QY 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRAPDTAVYYCTASGTFWPAWVGQGLTVTVSS 116
 DB 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRAPDTAVYYCTASGTFWPAWVGQGLTVTVSS 120

RESULT 12
 ADD35374
 ID ADD35374 standard; protein; 120 AA.
 AC ADD35374;

XX 15-JAN-2004 (first entry)
 DT
 XX
 XX Human MAB4D5-8 heavy chain variable domain SEQ ID NO:2.
 DE
 XX
 XX antibody heavy chain variable domain; hypervariable region; HER2 binding;
 KW humanised anti-HER2 antibody; cytostatic; antiinflammatory;
 KW immunosuppressive; gene therapy; cancer; breast cancer; tumour;
 KW leukaemia; lymphoid malignancy.

XX OS Homo sapiens.
XX PN WO2003087131-A2.
XX PD 23-OCT-2003.
XX PF 09-APR-2003; 2003WO-US011031.
XX PR 10-APR-2002; 2002US-0371609P.
XX PA (GETH) GENENTECH INC.
XX PI Lowman HB, Gershtner RB, Carter PJ;
XX WP1; 2003-845297/78.
XX
XX PT New polypeptide comprising an antibody light or heavy chain variable
XX PT variants, specifically anti-HER2 antibody variants, useful for treating
XX PT cancer, tumor, inflammatory, immunologic or angiogenic disorders.
XX
XX Claim 14; SEQ ID NO 2; 96pp; English.
XX
XX The present invention describes a polypeptide (I) comprising an antibody
XX light chain variable domain having hypervariable regions of a sequence of
XX 109 amino acids (P1, seeADJ3573), where one or more amino acids selected
XX from Q27(VL), D28(VL), N30(VL), T31(VL), A32(VL), Y49(VL), F53(VL),
XX Y55(VL), R66(VL), H91(VL), Y92(VL), and T94(VL), numbered according to
XX the Kabat numbering system, are substituted with any amino acid other
XX than alanine. Also described: (1) an antibody that is capable of binding
XX to the extracellular domain of HER2, which comprises the hypervariable
XX regions P1 and/or P2 (see ADJ3574); (2) a humanised anti-HER2 antibody
XX comprising one or more of the substitutions described above; (3) an
XX article of manufacture comprising a container, a composition contained in
XX it, and a package insert or label indicating that the composition can be
XX used to treat cancer characterised by the overexpression of HER2, where
XX the composition comprises the antibody described above; (4) an antibody
XX variant of a parent antibody which binds HER2, comprising an amino acid
XX substitution at position 98 of its heavy chain variable domain, and where
XX the binding affinity of the antibody variant for HER2 is better than the
XX binding affinity of the parent antibody for HER2; and (5) isolating high-
XX affinity variants of humanised anti-HER2 antibody. (1) has cytostatic,
XX antiinflammatory and immunosuppressive activities, and can be used in
XX gene therapy. The polypeptide and compositions are useful for treating
XX cancer, e.g. breast cancer, benign or malignant tumours, leukaemias and
XX lymphoid malignancies, and other disorders such as neural, glial,
XX astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal,
XX blastocoealic, inflammatory, angiogenic, and immunologic disorders. The
XX CC present sequence represent the heavy chain variable domain of humAb4D5-8,
XX which is used in the exemplification of the present invention.
XX
XX SQ Sequence 120 AA;
XX
XX Query Match 84.0%; Score 518; DB 7; Length 120;
XX Best Local Similarity 85.8%; Pred. No. 1.4e-38;
XX Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;
XX
XX QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTIY 60
XX DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIPYNGTRY 60
XX
XX QY 61 ADSYKGRFTTISDDSKNTAYLQNNSLRAEDPAVYYCTASG----YWPAYWGQGLTVTVSS 116
XX DB 61 ADSYKGRFTTISDDSKNTAYLQNNSLRAEDPAVYYCTASG----YWPAYWGQGLTVTVSS 120
XX
XX RESULT 13
XX ADC26167 standard; protein, 228 AA.
XX AC ADC26167;
XX DT 18-DEC-2003 (first entry)

XX DE Humanised anti-HER2 antibody 4D5 heavy chain variable domain protein.
XX KW antibody variant; cytostatic; cancer; heavy chain variable domain; 4D5;
XX KW anti-HER2; human.
XX OS Unidentified.
XX OS Homo sapiens.
XX PN WO2003068801-A2.
XX PD 21-AUG-2003.
XX PF 11-FEB-2003; 2003WO-US004184.
XX PR 11-FEB-2002; 2002US-0355895P.
XX PR 10-SEP-2002; 2002US-0409685P.
XX PA (GETH) GENENTECH INC.
XX PI Lowman HB, Marvin JS;
XX WP1; 2003-697521/66.
XX
XX PT Making an antibody variant of a parent antibody specific to an antigen by
XX PT identifying a target amino acid residue within the variable domain of the
XX PT parent antibody and substituting the target residue with a different
XX PT amino acid residue.
XX
XX Claim 35; SEQ ID NO 14; 81pp; English.
XX
XX The invention relates to a novel method for making an antibody variant of
XX a parent antibody specific to an antigen. This is achieved via
XX identifying a target amino acid residue within the variable domain of the
XX CC parent antibody and substituting the target residue with a different
XX CC replacement amino acid residue such that the charge complementarity
XX CC between the antibody and antigen is increased. The antibody variant of
XX the invention demonstrates cytostatic activity whilst the method may be
XX useful for treating cancer. The current sequence is that of the humanised
XX anti-HER2 antibody 4D5 heavy chain variable domain protein of the
XX invention.
XX
XX SQ Sequence 228 AA;
XX
XX Query Match 84.0%; Score 518; DB 7; Length 228;
XX Best Local Similarity 85.8%; Pred. No. 2.8e-38;
XX Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;
XX
XX QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTIY 60
XX DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIPYNGTRY 60
XX
XX QY 61 ADSYKGRFTTISDDSKNTAYLQNNSLRAEDPAVYYCTASG----YWPAYWGQGLTVTVSS 116
XX DB 61 ADSYKGRFTTISDDSKNTAYLQNNSLRAEDPAVYYCTASG----YWPAYWGQGLTVTVSS 120
XX
XX RESULT 14
XX AAB28158 standard; protein, 252 AA.
XX ID AAB28158
XX AC AAB28158;
XX DT 08-FEB-2001 (first entry)
XX DE Human anti-c-ErbB2 single chain Fv fragment 4D5.
XX KW Human; immunoglobulin; antigen-binding; framework region; carcinoma;
XX KW c-ErbB2; carcinoma-associated antigen.
XX OS Homo sapiens.
XX PN WO200061635-A2.

XX 19-OCT-2000.
 PD 10-APR-2000; 2000WO-EP003176.
 PF 09-APR-1999; 99EP-00107030.
 XX (UYZU-) UNIV ZUERICH.
 PA (PLUE/) PLUECKTHUN A.
 XX Plueckthun A, Honegger A, Willuda J;
 PI WPI; 2000-679468/66.
 DR Stabilizing chimeric immunoglobulin (Ig) involves setting up a stabilized
 PT antigen binding Ig or its fragment by replacing one or more residues
 PT present in acceptor Ig by those residues present in donor Ig.
 XX Claim 5; Page 51; 51pp; English.
 PS The present invention relates to a method for stabilizing a chimeric
 CC immunoglobulin (Ig). The method comprises identifying antigen-binding
 CC groups derived from donor Ig and framework regions derived from an
 CC acceptor Ig. The present sequence is one such acceptor Ig fragment. One
 CC or more of the residues present at the positions in the present sequence
 CC are replaced by those present at the corresponding positions in the donor
 CC Ig, after comparing the structural features of the VH domains of the
 CC acceptor Ig and the donor Ig. The method of the present invention is
 CC useful for producing a pharmaceutical composition which can be used for
 CC treating human carcinomas, since c-erbB2 is a carcinoma-associated
 CC antigen
 CC
 SQ Sequence 252 AA;
 Query Match 84.0%; Score 518; DB 3; Length 252;
 Best Local Similarity 85.8%; Pred. No. 3.1e-38;
 Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;
 QY 1 EVOLVESGGGLVPGGSLRLSCAASGPNIKDTYTHWRQAPGKGLEWVARIDPANDNTIY 60
 DB 133 EVOLVESGGGLVPGGSLRLSCAASGPNIKDTYTHWRQAPGKGLEWVARIDPANDNTIY 192
 QY 61 ADSVKGFTTSSDSSKNTAYLQWNSLRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 116
 DB 193 ADSVKGFTTSSDSSKNTAYLQWNSLRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 252

RESULT 15
 ADB85320
 ID ADB85320 standard; protein; 449 AA.
 AC ADB85320;
 XX
 DT 04-DEC-2003 (first entry)
 DE Heavy chain of the humanised anti-HER2 antibody, Herceptin/Trastuzumab.
 XX
 KM CH2/CH2; protein A chromatography; protein purification; antibody; HER-2;
 KM Herceptin; Trastuzumab; heavy chain.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 PN US2003153735-A1.
 XX
 PD 14-AUG-2003.
 PF 03-FEB-2003; 2003US-00356974.
 PR 05-FEB-2002; 2002US-0354579P.
 PA (GETH) GENENTECH INC.
 XX

PI Breese TN, Fahrner RL, Gorrell JR, Lazareschi KP, Lester PM;
 PI Peng D;
 DR WPI; 2003-678834/64.
 XX
 PT Purifying proteins by Protein A chromatography without using toxic
 PT chemicals, comprises removing contaminants by washing the solid phase
 PT with intermediate buffers e.g. detergent and salt.
 XX
 PS Disclosure; Fig 1B; 24pp; English.
 XX
 CC The invention relates to purifying a protein, which comprises a CH2/CH2
 CC region, from a contaminated solution by Protein A chromatography
 CC comprising: (1) adsorbing the protein to immobilized Protein A; (2)
 CC removing contaminants by washing the solid phase with a composition
 CC comprising: (a) detergent and salt; (b) a buffer at a concentration
 CC greater than 0.8 M; (c) salt and solvent; or (d) salt and a polymer; and
 CC (3) recovering the protein from the solid phase. The method is used to
 CC purify proteins, especially anti-HER (e.g. Herceptin/Trastuzumab) and
 CC anti-IGF antibodies and immunoadhesins. The intermediate wash buffers
 CC used remove contaminants without removing significant amounts of the
 CC protein of interest bound to Protein A. In addition the methods avoid the
 CC use of prior art chemicals such as tetramethylammonium chloride which is
 CC difficult to handle and dispense, toxic, requires costly disposal as
 CC hazardous waste and is corrosive at high concentration and low pH. The
 CC present sequence is the heavy chain of the humanised anti-HER2 antibody,
 CC Herceptin/Trastuzumab.
 CC
 SQ Sequence 449 AA;
 Query Match 84.0%; Score 518; DB 7; Length 449;
 Best Local Similarity 85.8%; Pred. No. 5.7e-38;
 Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;
 QY 1 EVOLVESGGGLVPGGSLRLSCAASGPNIKDTYTHWRQAPGKGLEWVARIDPANDNTIY 60
 DB 1 EVOLVESGGGLVPGGSLRLSCAASGPNIKDTYTHWRQAPGKGLEWVARIDPANDNTIY 60
 QY 61 ADSVKGFTTSSDSSKNTAYLQWNSLRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 116
 DB 61 ADSVKGFTTSSDSSKNTAYLQWNSLRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 120

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